

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Malcolm, Bruce  
Taremi, Shahriar S.  
Weber, Patricia  
Yao, Nanhua
- (ii) TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus  
NS3 Protease and NS4A Cofactor Peptide
- (iii) NUMBER OF SEQUENCES: 123
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Schering-Plough Corp.  
(B) STREET: 2000 Galloping Hill Road  
(C) CITY: Kenilworth  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07030
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Power Macintosh  
(C) OPERATING SYSTEM: 8.0.1  
(D) SOFTWARE: Microsoft Word 6.0.1
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: McLaughlin, Jaye P.  
(B) REGISTRATION NUMBER: 41,211  
(C) REFERENCE/DOCKET NUMBER: JB0800P2
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (908)298-5056  
(B) TELEFAX: (908)298-5388

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 217 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

SECRET  
Sub  
A1

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 217 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu

20 25 30  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35 40 45  
 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 50 55 60  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 65 70 75 80  
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 85 90 95  
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 100 105 110  
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
 115 120 125  
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 Ser Met Glu Thr Thr Met Arg Ser \*  
 210 215

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

CCNCCFEEZBETED

(2) INFORMATION FOR SEQ ID NO:4:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Cys | Lys | Lys | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |



50                      55                      60  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 65                      70                      75                      80  
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 85                      90                      95  
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 100                      105                      110  
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
 115                      120                      125  
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130                      135                      140  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145                      150                      155                      160  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165                      170                      175  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180                      185                      190  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195                      200                      205  
 Ser Met Glu Thr Thr Met Arg Ser \*  
 210                      215

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1                      5                      10                      15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20                      25                      30  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35                      40                      45  
 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 50                      55                      60  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala

(2) INFORMATION FOR SEQ ID NO:6:

(A) LENGTH: 216 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Cys | Lys | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser |

(2) INFORMATION FOR SEO ID NO:7:

(A) LENGTH: 217 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Cys | Ile | Lys | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn |

|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 100   |     | 105 |     | 110 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser | 115 | 120 |     | 125 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg | 130 | 135 |     | 140 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser | 145 | 150 | 155 | 160 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly | 165 | 170 |     | 175 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala | 180 | 185 |     | 190 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu | 195 | 200 |     | 205 |
| Ser Met Glu Thr Thr Met Arg Ser *                               | 210 | 215 |     |     |

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|   |     |     |     |    |
|---|-----|-----|-----|----|
| Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro     | 1   | 5   | 10  | 15 |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu | 20  | 25  | 30  |    |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu | 35  | 40  | 45  |    |
| Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val | 50  | 55  | 60  |    |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala | 65  | 70  | 75  | 80 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser | 85  | 90  | 95  |    |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn | 100 | 105 | 110 |    |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Ala | Gly | Gly | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Cys | Ile | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 Ser Met Glu Thr Thr Met Arg Ser \*  
 210 215

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35 40 45  
 Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 50 55 60  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 65 70 75 80  
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 85 90 95  
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 100 105 110  
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
 115 120 125  
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160

Sequence: EC266160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser  
 210 215 220  
 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro  
 225 230 235 240  
 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln  
 245 250 255  
 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly  
 260 265 270  
 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg  
 275 280 285  
 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr  
 290 295 300  
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp  
 305 310 315 320  
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu  
 325 330 335  
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu  
 340 345 350  
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His  
 355 360 365  
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe  
 370 375 380  
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu  
 385 390 395 400  
 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu  
 405 410 415  
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr

110112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100



(2) INFORMATION FOR SEQ ID NO:12:

(A) LENGTH: 665 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
  1          5          10          15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
      20          25          30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

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|   |     |     |
|---|-----|-----|
| 35  | 40  | 45  |
| Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |     |
| 50  | 55  | 60  |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |     |
| 65  | 70  | 75  |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |     |
|   | 85  | 90  |
|   |     | 95  |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |     |
|   | 100 | 105 |
|   |     | 110 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |     |
|   | 115 | 120 |
|   |     | 125 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |     |
|   | 130 | 135 |
|   |     | 140 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |     |
| 145   | 150 | 155 |
|   |     | 160 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly |     |     |
|   | 165 | 170 |
|   |     | 175 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |     |
|   | 180 | 185 |
|   |     | 190 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |     |
|   | 195 | 200 |
|   |     | 205 |
| Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser |     |     |
|   | 210 | 215 |
|   |     | 220 |
| Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro |     |     |
| 225   | 230 | 235 |
|   |     | 240 |
| Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln |     |     |
|   | 245 | 250 |
|   |     | 255 |
| Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly |     |     |
|   | 260 | 265 |
|   |     | 270 |
| Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg |     |     |
|   | 275 | 280 |
|   |     | 285 |
| Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr |     |     |
|   | 290 | 295 |
|   |     | 300 |
| Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp |     |     |
| 305   | 310 | 315 |
|   |     | 320 |
| Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu |     |     |
|   | 325 | 330 |
|   |     | 335 |
| Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu |     |     |
|   | 340 | 345 |
|   |     | 350 |

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His  
 355 360 365  
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe  
 370 375 380  
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu  
 385 390 395 400  
 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu  
 405 410 415  
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr  
 465 470 475 480  
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655

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Cys Met Ser Ala Asp Leu Glu Val Val  
660 665

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
35 40 45

Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
50 55 60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
65 70 75 80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
85 90 95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
100 105 110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
115 120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
130 135 140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
145 150 155 160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
165 170 175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
180 185 190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
195 200 205

Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser  
210 215 220

Sequence: 665

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro  
 225 230 235 240  
 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln  
 245 250 255  
 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly  
 260 265 270  
 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg  
 275 280 285  
 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr  
 290 295 300  
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp  
 305 310 315 320  
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu  
 325 330 335  
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu  
 340 345 350  
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His  
 355 360 365  
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe  
 370 375 380  
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu  
 385 390 395 400  
 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu  
 405 410 415  
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr  
 465 470 475 480  
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr

330  
 320  
 310  
 300  
 290  
 280  
 270  
 260  
 250  
 240  
 230  
 225

530                                      535                                      540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545                                      550                                      555                                      560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
                                     565                                      570                                      575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
                                     580                                      585                                      590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
                                     595                                      600                                      605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
                                     610                                      615                                      620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625                                      630                                      635                                      640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
                                     645                                      650                                      655  
 Cys Met Ser Ala Asp Leu Glu Val Val  
                                     660                                      665

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1                                      5                                      10                                      15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
                                     20                                      25                                      30  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
                                     35                                      40                                      45  
 Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
                                     50                                      55                                      60  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 65                                      70                                      75                                      80  
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
                                     85                                      90                                      95  
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn

|  |     |     |
|--|-----|-----|
| 100  | 105 | 110 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser<br>115 120 125     |     |     |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg<br>130 135 140     |     |     |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser<br>145 150 155 160 |     |     |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly<br>165 170 175     |     |     |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala<br>180 185 190     |     |     |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu<br>195 200 205     |     |     |
| Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser<br>210 215 220     |     |     |
| Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro<br>225 230 235 240 |     |     |
| Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln<br>245 250 255     |     |     |
| Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly<br>260 265 270     |     |     |
| Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg<br>275 280 285     |     |     |
| Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr<br>290 295 300     |     |     |
| Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp<br>305 310 315 320 |     |     |
| Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu<br>325 330 335     |     |     |
| Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu<br>340 345 350     |     |     |
| Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His<br>355 360 365     |     |     |
| Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe<br>370 375 380     |     |     |
| Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu<br>385 390 395 400 |     |     |
| Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu<br>405 410 415     |     |     |

SECRET = E2230160

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr  
 465 470 475 480  
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655  
 Cys Met Ser Ala Asp Leu Glu Val Val  
 660 665

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Sequence = E226160



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Gly        | Ser        | Ser        | His<br>5   | His        | His        | His        | His<br>10  | Ser        | Ser        | Gly        | Leu        | Val        | Pro        |            |
| Arg        | Gly        | Ser        | His<br>20  | Met        | Gly        | Ser        | Val        | Val<br>25  | Ile        | Val        | Gly        | Arg        | Ile<br>30  | Ile        | Leu        |
| Ser        | Gly        | Ser<br>35  | Gly        | Ser        | Ile        | Thr        | Ala<br>40  | Tyr        | Ser        | Gln        | Gln        | Thr<br>45  | Arg        | Gly        | Leu        |
| Leu        | Gly<br>50  | Cys        | Ile        | Ile        | Thr        | Ser<br>55  | Leu        | Thr        | Gly        | Arg        | Asp<br>60  | Lys        | Asn        | Gln        | Val        |
| Glu<br>65  | Gly        | Glu        | Val        | Gln        | Val<br>70  | Val        | Ser        | Thr        | Ala        | Thr<br>75  | Gln        | Ser        | Phe        | Leu        | Ala<br>80  |
| Thr        | Cys        | Val        | Asn<br>85  | Gly        | Val        | Cys        | Trp        | Thr        | Val<br>90  | Tyr        | His        | Gly        | Ala        | Gly<br>95  | Ser        |
| Lys        | Thr        | Leu        | Ala<br>100 | Gly        | Pro        | Lys        | Gly        | Pro<br>105 | Ile        | Thr        | Gln        | Met        | Tyr<br>110 | Thr        | Asn        |
| Val        | Asp        | Gln<br>115 | Asp        | Leu        | Val        | Gly        | Trp<br>120 | Gln        | Ala        | Pro        | Pro        | Gly<br>125 | Ala        | Arg        | Ser        |
| Leu        | Thr<br>130 | Pro        | Cys        | Thr        | Cys        | Gly<br>135 | Ser        | Ser        | Asp        | Leu        | Tyr<br>140 | Leu        | Val        | Thr        | Arg        |
| His<br>145 | Ala        | Asp        | Val        | Ile        | Pro<br>150 | Val        | Arg        | Arg        | Arg        | Gly<br>155 | Asp        | Ser        | Arg        | Gly        | Ser<br>160 |
| Leu        | Leu        | Ser        | Pro        | Arg<br>165 | Pro        | Val        | Ser        | Tyr        | Leu<br>170 | Lys        | Gly        | Ser        | Ala        | Gly<br>175 | Gly        |
| Pro        | Leu        | Leu        | Cys<br>180 | Pro        | Ser        | Gly        | His        | Ala<br>185 | Val        | Gly        | Ile        | Phe        | Arg<br>190 | Ala        | Ala        |
| Val        | Cys<br>195 | Thr        | Arg        | Gly        | Val        | Ala        | Lys<br>200 | Ala        | Val        | Asp        | Phe        | Val<br>205 | Pro        | Val        | Glu        |
| Ser        | Met<br>210 | Glu        | Thr        | Thr        | Met        | Arg<br>215 | Ser        | Pro        | Val        | Phe        | Thr<br>220 | Asp        | Asn        | Ser        | Ser        |
| Pro<br>225 | Pro        | Ala        | Val        | Pro        | Gln<br>230 | Ser        | Phe        | Gln        | Val        | Ala<br>235 | His        | Leu        | His        | Ala        | Pro<br>240 |
| Thr        | Gly        | Ser        | Gly<br>245 | Lys        | Ser        | Thr        | Lys        | Val        | Pro<br>250 | Ala        | Ala        | Tyr        | Ala<br>255 | Ala        | Gln        |
| Gly        | Tyr        | Lys        | Val<br>260 | Leu        | Val        | Leu        | Asn        | Pro<br>265 | Ser        | Val        | Ala        | Ala        | Thr<br>270 | Leu        | Gly        |
| Phe        | Gly        | Ala<br>275 | Tyr        | Met        | Ser        | Lys        | Ala<br>280 | His        | Gly        | Ile        | Asp<br>285 | Pro        | Asn        | Ile        | Arg        |

Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr  
 290 295 300  
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp  
 305 310 315 320  
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu  
 325 330 335  
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu  
 340 345 350  
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His  
 355 360 365  
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe  
 370 375 380  
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu  
 385 390 395 400  
 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu  
 405 410 415  
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr  
 465 470 475 480  
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala

(2) INFORMATION FOR SEQ ID NO:16:

(A) LENGTH: 665 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Cys | Lys | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ala | Gly | Gly |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|------------|-----|
|            |            |            |            | 165        |            |            |            |            |            | 170        |            |            |            |     |            | 175 |
| Pro        | Leu        | Leu        | Cys<br>180 | Pro        | Ser        | Gly        | His        | Ala<br>185 | Val        | Gly        | Ile        | Phe        | Arg<br>190 | Ala | Ala        |     |
| Val        | Cys        | Thr<br>195 | Arg        | Gly        | Val        | Ala        | Lys<br>200 | Ala        | Val        | Asp        | Phe        | Val<br>205 | Pro        | Val | Glu        |     |
| Ser        | Met<br>210 | Glu        | Thr        | Thr        | Met        | Arg<br>215 | Ser        | Pro        | Val        | Phe        | Thr<br>220 | Asp        | Asn        | Ser | Ser        |     |
| Pro<br>225 | Pro        | Ala        | Val        | Pro        | Gln<br>230 | Ser        | Phe        | Gln        | Val        | Ala<br>235 | His        | Leu        | His        | Ala | Pro<br>240 |     |
| Thr        | Gly        | Ser        | Gly        | Lys<br>245 | Ser        | Thr        | Lys        | Val        | Pro<br>250 | Ala        | Ala        | Tyr        | Ala        | Ala | Gln<br>255 |     |
| Gly        | Tyr        | Lys        | Val<br>260 | Leu        | Val        | Leu        | Asn        | Pro<br>265 | Ser        | Val        | Ala        | Ala        | Thr<br>270 | Leu | Gly        | .   |
| Phe        | Gly        | Ala<br>275 | Tyr        | Met        | Ser        | Lys        | Ala<br>280 | His        | Gly        | Ile        | Asp        | Pro<br>285 | Asn        | Ile | Arg        |     |
| Thr<br>290 | Gly        | Val        | Arg        | Thr        | Ile        | Thr<br>295 | Thr        | Gly        | Ala        | Pro        | Val<br>300 | Thr        | Tyr        | Ser | Thr        |     |
| Tyr<br>305 | Gly        | Lys        | Phe        | Leu        | Ala<br>310 | Asp        | Gly        | Gly        | Cys        | Ser<br>315 | Gly        | Gly        | Ala        | Tyr | Asp<br>320 |     |
| Ile        | Ile        | Ile        | Cys        | Asp<br>325 | Glu        | Cys        | His        | Ser        | Thr<br>330 | Asp        | Ser        | Thr        | Thr        | Ile | Leu<br>335 |     |
| Gly        | Ile        | Gly        | Thr<br>340 | Val        | Leu        | Asp        | Gln        | Ala<br>345 | Glu        | Thr        | Ala        | Gly        | Ala        | Arg | Leu        |     |
| Val        | Val        | Leu<br>355 | Ala        | Thr        | Ala        | Thr        | Pro<br>360 | Pro        | Gly        | Ser        | Val        | Thr<br>365 | Val        | Pro | His        |     |
| Pro<br>370 | Asn        | Ile        | Glu        | Glu        | Val        | Ala<br>375 | Leu        | Ser        | Asn        | Thr        | Gly<br>380 | Glu        | Ile        | Pro | Phe        |     |
| Tyr<br>385 | Gly        | Lys        | Ala        | Ile        | Pro<br>390 | Ile        | Glu        | Ala        | Ile        | Arg<br>395 | Gly        | Gly        | Arg        | His | Leu<br>400 |     |
| Ile        | Phe        | Cys        | His        | Ser<br>405 | Lys        | Lys        | Lys        | Cys        | Asp<br>410 | Glu        | Leu        | Ala        | Ala        | Lys | Leu<br>415 |     |
| Ser        | Gly        | Leu        | Gly<br>420 | Ile        | Asn        | Ala        | Val        | Ala<br>425 | Tyr        | Tyr        | Arg        | Gly        | Leu        | Asp | Val        |     |
| Ser        | Val        | Ile<br>435 | Pro        | Thr        | Ile        | Gly        | Asp<br>440 | Val        | Val        | Val        | Val        | Ala<br>445 | Thr        | Asp | Ala        |     |
| Leu<br>450 | Met        | Thr        | Gly        | Tyr        | Thr        | Gly<br>455 | Asp        | Phe        | Asp        | Ser        | Val<br>460 | Ile        | Asp        | Cys | Asn        |     |
| Thr<br>465 | Cys        | Val        | Thr        | Gln        | Thr        | Val        | Asp        | Phe        | Ser        | Leu<br>475 | Asp        | Pro        | Thr        | Phe | Thr<br>480 |     |

(2) INFORMATION FOR SEQ ID NO:17:

(A) LENGTH: 665 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
20 25 30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
35 40 45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Cys | Ile | Lys | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | 50  | 55  | 60  |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala | 65  | 70  | 75  |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser | 85  | 90  | 95  |
| Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn | 100 | 105 | 110 |
| Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser | 115 | 120 | 125 |
| Leu | Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg | 130 | 135 | 140 |
| His | Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser | 145 | 150 | 155 |
| Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ala | Gly | Gly | 165 | 170 | 175 |
| Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala | 180 | 185 | 190 |
| Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val | Asp | Phe | Val | Pro | Val | Glu | 195 | 200 | 205 |
| Ser | Met | Glu | Thr | Thr | Met | Arg | Ser | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser | 210 | 215 | 220 |
| Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro | 225 | 230 | 235 |
| Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln | 245 | 250 | 255 |
| Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly | 260 | 265 | 270 |
| Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg | 275 | 280 | 285 |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr | 290 | 295 | 300 |
| Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | 305 | 310 | 315 |
| Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu | 325 | 330 | 335 |
| Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu | 340 | 345 | 350 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Ser | Val | Arg | Leu | Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Gln | Asp | His | Leu | Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Ile | Asp | Ala | His | Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Pro | Tyr | Leu | Val | Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Pro | Pro | Pro | Ser | Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys |
|     |     |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Pro | Thr | Leu | His | Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Gln | Asn | Glu | Val | Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Cys | Met | Ser | Ala | Asp | Leu | Glu | Val | Val |     |     |     |     |     |     |     |

660

665

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1             5             10             15
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu.
          20             25             30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
          35             40             45
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
          50             55             60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
          65             70             75             80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
          85             90             95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
          100            105            110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
          115            120            125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
          130            135            140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
          145            150            155            160
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
          165            170            175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
          180            185            190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
          195            200            205
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser
          210            215            220
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro

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| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |
| Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 | 320 |
| Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu |
|     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |
| Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His |
|     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |
|     |     |     |     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |
|     |     |     |     | 385 |     |     |     |     | 390 |     |     |     |     | 395 | 400 |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |
|     |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |
|     |     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |
|     |     |     |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |
|     |     |     |     | 465 |     |     |     |     | 470 |     |     |     |     | 475 | 480 |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |
| Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |
| Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655  
 Cys Met Ser Ala Asp Leu Glu Val Val  
 660 665

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile  
 20 25 30  
 Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser  
 35 40 45  
 Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly  
 50 55 60  
 Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala  
 65 70 75 80  
 Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val  
 85 90 95  
 Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile  
 100 105 110

Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala  
 115 120 125  
 Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp  
 130 135 140  
 Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg  
 145 150 155 160  
 Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu  
 165 170 175  
 Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala Val  
 180 185 190  
 Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala Val  
 195 200 205  
 Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro Val  
 210 215 220  
 Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Ser Phe Gln Val  
 225 230 235 240  
 Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro  
 245 250 255  
 Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser  
 260 265 270  
 Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly  
 275 280 285  
 Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala  
 290 295 300  
 Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys  
 305 310 315 320  
 Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr  
 325 330 335  
 Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu  
 340 345 350  
 Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly  
 355 360 365  
 Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn  
 370 375 380  
 Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile  
 385 390 395 400  
 Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp  
 405 410 415

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Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr  
                   420                                  425                                  430  
 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val  
                   435                                  440                                  445  
 Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp  
                   450                                  455                                  460  
 Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser  
                   465                                  470                                  475                                  480  
 Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala  
                                   485                                  490                                  495  
 Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly  
                                   500                                  505                                  510  
 Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp  
                   515                                  520                                  525  
 Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu  
                   530                                  535                                  540  
 Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr  
                   545                                  550                                  555                                  560  
 Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val  
                                   565                                  570                                  575  
 Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys  
                   580                                  585                                  590  
 Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val  
                   595                                  600                                  605  
 Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys  
                   610                                  615                                  620  
 Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu  
                   625                                  630                                  635                                  640  
 Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile  
                   645                                  650                                  655  
 Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val  
                   660                                  665                                  670

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 671 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro | 1   | 5   | 10  | 15  |     |     |
| Arg | Gly | Ser | His | Met | Ala | Tyr | Ser | Leu | Thr | Thr | Gly | Ser | Val | Val | Ile | 20  | 25  | 30  |     |
| Val | Gly | Arg | Ile | Ile | Leu | Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | 35  | 40  | 45  |     |
| Gln | Gln | Thr | Arg | Gly | Leu | Leu | Gly | Cys | Ile | Ile | Thr | Ser | Leu | Thr | Gly | 50  | 55  | 60  |     |
| Arg | Asp | Lys | Asn | Gln | Val | Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | 65  | 70  | 75  | 80  |
| Thr | Gln | Ser | Phe | Leu | Ala | Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | 85  | 90  | 95  |     |
| Tyr | His | Gly | Ala | Gly | Ser | Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | 100 | 105 | 110 |     |
| Thr | Gln | Met | Tyr | Thr | Asn | Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | 115 | 120 | 125 |     |
| Pro | Pro | Gly | Ala | Arg | Ser | Leu | Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp | 130 | 135 | 140 |     |
| Leu | Tyr | Leu | Val | Thr | Arg | His | Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg | 145 | 150 | 155 | 160 |
| Gly | Asp | Ser | Arg | Gly | Ser | Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu | 165 | 170 | 175 |     |
| Lys | Gly | Ser | Ala | Gly | Gly | Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val | 180 | 185 | 190 |     |
| Gly | Ile | Phe | Arg | Ala | Ala | Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val | 195 | 200 | 205 |     |
| Asp | Phe | Val | Pro | Val | Glu | Ser | Met | Glu | Thr | Thr | Met | Arg | Ser | Pro | Val | 210 | 215 | 220 |     |
| Phe | Thr | Asp | Asn | Ser | Ser | Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val | 225 | 230 | 235 | 240 |
| Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | 245 | 250 | 255 |     |
| Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | 260 | 265 | 270 |     |
| Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | 275 | 280 | 285 |     |
| Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|-----|
| 290 |     |     |     |     |     |     |     |     |     |     | 295 |     |     |     |     |  |  |  |  |  |  | 300 |
| Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys |  |  |  |  |  |  |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |  |  |     |
| Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr |  |  |  |  |  |  |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |  |  |     |
| Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu |  |  |  |  |  |  |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |  |  |     |
| Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly |  |  |  |  |  |  |     |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |  |  |     |
| Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn |  |  |  |  |  |  |     |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |  |  |     |
| Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile |  |  |  |  |  |  |     |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |  |  |     |
| Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp |  |  |  |  |  |  |     |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |  |  |     |
| Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr |  |  |  |  |  |  |     |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |  |  |  |  |     |
| Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val |  |  |  |  |  |  |     |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |  |  |     |
| Val | Val | Ala | Thr | Asp | Ala | Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp |  |  |  |  |  |  |     |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |  |  |     |
| Ser | Val | Ile | Asp | Cys | Asn | Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser |  |  |  |  |  |  |     |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |  |  |  |  |     |
| Leu | Asp | Pro | Thr | Phe | Thr | Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala |  |  |  |  |  |  |     |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |  |  |  |  |     |
| Val | Ser | Arg | Ser | Gln | Arg | Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly |  |  |  |  |  |  |     |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |  |  |  |  |     |
| Ile | Tyr | Arg | Phe | Val | Thr | Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp |  |  |  |  |  |  |     |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |  |  |  |  |     |
| Ser | Ser | Val | Leu | Cys | Glu | Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu |  |  |  |  |  |  |     |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |  |  |  |  |     |
| Leu | Thr | Pro | Ala | Glu | Thr | Ser | Val | Arg | Leu | Arg | Ala | Tyr | Leu | Asn | Thr |  |  |  |  |  |  |     |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |  |  |  |  |     |
| Pro | Gly | Leu | Pro | Val | Cys | Gln | Asp | His | Leu | Glu | Phe | Trp | Glu | Ser | Val |  |  |  |  |  |  |     |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |  |  |  |  |     |
| Phe | Thr | Gly | Leu | Thr | His | Ile | Asp | Ala | His | Phe | Leu | Ser | Gln | Thr | Lys |  |  |  |  |  |  |     |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |  |  |  |  |  |     |
| Gln | Ala | Gly | Asp | Asn | Phe | Pro | Tyr | Leu | Val | Ala | Tyr | Gln | Ala | Thr | Val |  |  |  |  |  |  |     |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |  |  |  |  |  |     |

(2) INFORMATION FOR SEQ ID NO:21:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21;

(2) INFORMATION FOR SEQ ID NO:22:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

(2) INFORMATION FOR SEQ ID NO:22:

(ii) MOLECULE TYPE: cDNA







Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp  
 515 520 525  
 His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp  
 530 535 540  
 Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr  
 545 550 555 560  
 Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro  
 565 570 575  
 Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr  
 580 585 590  
 Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn  
 595 600 605  
 Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met  
 610 615 620  
 Ser Ala Asp Leu Glu Val Val Thr  
 625 630

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr  
 1 5 10 15  
 Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu Ser  
 20 25 30  
 Gly Arg Pro Ala Ile Val Pro Asp Arg Glu Leu Leu Tyr Gln Glu Phe  
 35 40 45  
 Asp Glu Met Glu Glu Cys  
 50

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

(2) INFORMATION FOR SEQ ID NO:26:

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTGG TAGTGGTAGT 60

ATCACGGCCT ACTCCCAA 78

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT 36

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG

39

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC

40

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCAGAGCAGT GGACCACCAG CAGAGCCCTT CAAGTAGGAG

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

Sequence: 39 bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:  
CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:  
GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:

367677-223010

- (ii) MOLECULE TYPE: cDNA

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTGGT  
ATCACGGCCT ACTCCCAA

78

(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

36

(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro | 1   | 5   | 10  | 15  |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu | 20  | 25  | 30  |     |
| Ser | Pro | Ala | Gly | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu | Leu | 35  | 40  | 45  |     |
| Gly | Cys | Ile | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | Glu | 50  | 55  | 60  |     |
| Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala | Thr | 65  | 70  | 75  | 80  |
| Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser | Lys | 85  | 90  | 95  |     |
| Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn | Val | 100 | 105 | 110 |     |
| Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser | Leu | 115 | 120 | 125 |     |
| Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg | His | 130 | 135 | 140 |     |
| Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser | Leu | 145 | 150 | 155 | 160 |
| Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ser | Gly | Gly | Pro | 165 | 170 | 175 |     |
| Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala | Val | 180 | 185 | 190 |     |

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser  
 195 200 205

Met Glu Thr Thr Met Arg Ser \*  
 210 215

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Ala Gly  
 1

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTATC 60  
 ACGGCCTACT CCCAA 75

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

36

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30

Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu  
 35 40 45

Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu  
 50 55 60

Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr  
 65 70 75 80

Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys  
 85 90 95

Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val  
 100 105 110

Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu  
 115 120 125

Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His  
 130 135 140

Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu  
 145 150 155 160

Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro  
 165 170 175

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val  
 180 185 190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser  
 195 200 205

Met Glu Thr Thr Met  
 210

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 166 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | Glu | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala | Thr | Cys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser | Lys | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn | Val | Asp | Gln |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |



## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

36

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu  
 35 40 45  
 Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu  
 50 55 60  
 Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr  
 65 70 75 80  
 Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys  
 85 90 95  
 Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val  
 100 105 110  
 Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu  
 115 120 125  
 Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His  
 130 135 140  
 Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu

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145                                      150                                      155                                      160  
 Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro  
    165                                      170                                      175  
 Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val  
    180                                      185                                      190  
 Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser  
    195                                      200                                      205  
 Met Glu Thr Thr Met Arg Ser \*  
    210                                      215

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 668 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala  
 1 5 10 15  
 Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys  
 20 25 30  
 Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val  
 35 40 45  
 Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn  
 50 55 60  
 Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala  
 65 70 75 80  
 Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp  
 85 90 95  
 Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys  
 100 105 110  
 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val  
 115 120 125  
 Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro  
 130 135 140  
 Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys  
 145 150 155 160  
 Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg  
 165 170 175  
 Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr  
 180 185 190  
 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val  
 195 200 205  
 Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly  
 210 215 220  
 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val  
 225 230 235 240  
 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr  
 245 250 255  
 Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg  
 260 265 270  
 Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe  
 275 280 285  
 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys  
 290 295 300  
 Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr

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305                      310                      315                      320  
 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala  
                                  325                      330                      335  
 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu  
                                  340                      345                      350  
 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala  
                                  355                      360                      365  
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His  
                                  370                      375                      380  
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly  
 385                                   390                      395                      400  
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro  
                                  405                      410                      415  
 Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly  
                                  420                      425                      430  
 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr  
                                  435                      440                      445  
 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr  
                                  450                      455                      460  
 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr  
 465                                   470                      475                      480  
 Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg  
                                  485                      490                      495  
 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala  
                                  500                      505                      510  
 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu  
                                  515                      520                      525  
 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu  
                                  530                      535                      540  
 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
 545                                   550                      555                      560  
 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val  
                                  565                      570                      575  
 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
                                  580                      585                      590  
 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His  
                                  595                      600                      605  
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val  
                                  610                      615                      620

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Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
625 630 635 640

Asp Leu Glu Val Val Thr \* Glu Phe Glu Leu Arg Arg Gln Ala Cys  
645 650 655

Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg  
660 665

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 668 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile | 20  | 25  | 30  |
| Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val | 35  | 40  | 45  |
| Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn | 50  | 55  | 60  |
| Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala | 65  | 70  | 75  |
| Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp | 85  | 90  | 95  |
| Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys | 100 | 105 | 110 |
| Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val | 115 | 120 | 125 |
| Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro | 130 | 135 | 140 |
| Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys | 145 | 150 | 155 |
| Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg | 165 | 170 | 175 |
| Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr | 180 | 185 | 190 |
| Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val | 195 | 200 | 205 |
| Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly | 210 | 215 | 220 |
| Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val | 225 | 230 | 235 |
| Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr | 245 | 250 | 255 |
| Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg | 260 | 265 | 270 |
| Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe | 275 | 280 | 285 |
| Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys | 290 | 295 | 300 |
| Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr | 305 | 310 | 315 |
|   |     |     | 320 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala | 325 | 330 | 335 |
| Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu | 340 | 345 | 350 |
| Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala | 355 | 360 | 365 |
| Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His | 370 | 375 | 380 |
| Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly | 385 | 390 | 400 |
| Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro | 405 | 410 | 415 |
| Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala | Leu | Met | Thr | Gly | 420 | 425 | 430 |
| Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn | Thr | Cys | Val | Thr | 435 | 440 | 445 |
| Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr | Ile | Glu | Thr | Thr | 450 | 455 | 460 |
| Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg | Arg | Gly | Arg | Thr | 465 | 470 | 480 |
| Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr | Pro | Gly | Glu | Arg | 485 | 490 | 495 |
| Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu | Cys | Tyr | Asp | Ala | 500 | 505 | 510 |
| Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr | Ser | Val | Arg | Leu | 515 | 520 | 525 |
| Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys | Gln | Asp | His | Leu | 530 | 535 | 540 |
| Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His | Ile | Asp | Ala | His | 545 | 550 | 555 |
| Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe | Pro | Tyr | Leu | Val | 565 | 570 | 575 |
| Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala | Pro | Pro | Pro | Ser | 580 | 585 | 590 |
| Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys | Pro | Thr | Leu | His | 595 | 600 | 605 |
| Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val | Gln | Asn | Glu | Val | 610 | 615 | 620 |



Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val  
 35 40 45  
 Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn  
 50 55 60  
 Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala  
 65 70 75 80  
 Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp  
 85 90 95  
 Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys  
 100 105 110  
 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val  
 115 120 125  
 Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro  
 130 135 140  
 Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys  
 145 150 155 160  
 Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg  
 165 170 175  
 Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr  
 180 185 190  
 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val  
 195 200 205  
 Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly  
 210 215 220  
 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val  
 225 230 235 240  
 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr  
 245 250 255  
 Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg  
 260 265 270  
 Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe  
 275 280 285  
 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys  
 290 295 300  
 Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr  
 305 310 315 320  
 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala  
 325 330 335

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Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu  
 340 345 350  
 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala  
 355 360 365  
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His  
 370 375 380  
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly  
 385 390 395 400  
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro  
 405 410 415  
 Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly  
 420 425 430  
 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr  
 435 440 445  
 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr  
 450 455 460  
 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr  
 465 470 475 480  
 Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg  
 485 490 495  
 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala  
 500 505 510  
 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu  
 515 520 525  
 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu  
 530 535 540  
 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
 545 550 555 560  
 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val  
 565 570 575  
 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
 580 585 590  
 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His  
 595 600 605  
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val  
 610 615 620  
 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
 625 630 635 640  
 Asp Leu Glu Val Val Thr \*

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## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC

40

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCAGAGCAGT GGACCACCAG CAGAGCCCTT CAAGTAGGAG

40

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 668 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Met | His | His | His | His | His | His | His | Leu | Val | Pro | Arg | Gly | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu | Leu | Gly | Cys | Ile |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | Glu | Gly | Glu | Val |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |





355 360 365  
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His  
 370 375 380  
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly  
 385 390 395 400  
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro  
 405 410 415  
 Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly  
 420 425 430  
 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr  
 435 440 445  
 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr  
 450 455 460  
 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr  
 465 470 475 480  
 Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg  
 485 490 495  
 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala  
 500 505 510  
 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu  
 515 520 525  
 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu  
 530 535 540  
 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
 545 550 555 560  
 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val  
 565 570 575  
 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
 580 585 590  
 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His  
 595 600 605  
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val  
 610 615 620  
 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
 625 630 635 640  
 Asp Leu Glu Val Val Thr \* Glu Phe Glu Leu Arg Arg Gln Ala Cys  
 645 650 655  
 Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg  
 660 665

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## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTCCGTCATA CCAACTTCCG GAGACGTCGT TGTCG

35

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGACAACGAC GTCTCCGGAA GTTGGTATGA CGGAC

35

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 669 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Met | His | His | His | His | His | His | His | Leu | Val | Pro | Arg | Gly | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu | Leu | Gly | Cys | Ile |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | Glu | Gly | Glu | Val |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala | Thr | Cys | Val | Asn |     |

|   |  |     |  |     |
|---|--|-----|--|-----|
| 50  |  | 55  |  | 60  |
| Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala |  |     |  |     |
| 65  |  | 70  |  | 75  |
|   |  |     |  | 80  |
| Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp |  |     |  |     |
|   |  | 85  |  | 90  |
|   |  |     |  | 95  |
| Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys |  |     |  |     |
|   |  | 100 |  | 105 |
|   |  |     |  | 110 |
| Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val |  |     |  |     |
|   |  | 115 |  | 120 |
|   |  |     |  | 125 |
| Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro |  |     |  |     |
|   |  | 130 |  | 135 |
|   |  |     |  | 140 |
| Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys |  |     |  |     |
|   |  | 145 |  | 150 |
|   |  |     |  | 155 |
| Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg |  |     |  |     |
|   |  | 165 |  | 170 |
|   |  |     |  | 175 |
| Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr |  |     |  |     |
|   |  | 180 |  | 185 |
|   |  |     |  | 190 |
| Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val |  |     |  |     |
|   |  | 195 |  | 200 |
|   |  |     |  | 205 |
| Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly |  |     |  |     |
|   |  | 210 |  | 215 |
|   |  |     |  | 220 |
| Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val |  |     |  |     |
|   |  | 225 |  | 230 |
|   |  |     |  | 235 |
| Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr |  |     |  |     |
|   |  | 245 |  | 250 |
|   |  |     |  | 255 |
| Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg |  |     |  |     |
|   |  | 260 |  | 265 |
|   |  |     |  | 270 |
| Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe |  |     |  |     |
|   |  | 275 |  | 280 |
|   |  |     |  | 285 |
| Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys |  |     |  |     |
|   |  | 290 |  | 295 |
|   |  |     |  | 300 |
| Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr |  |     |  |     |
|   |  | 305 |  | 310 |
|   |  |     |  | 315 |
| Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala |  |     |  |     |
|   |  | 325 |  | 330 |
|   |  |     |  | 335 |
| Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu |  |     |  |     |
|   |  | 340 |  | 345 |
|   |  |     |  | 350 |
| Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala |  |     |  |     |
|   |  | 355 |  | 360 |
|   |  |     |  | 365 |



- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACTAAAGTGC CGGCTGCCTA CGCAGCCCAA GGG

33

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCCTTGGGCT GCGTAGGCAG CCGGCACTTT AGT

33

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CCCTTGGGCT GCGTAGGCAG CCGGCACTTT AGT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGG

38

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG

39

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG



39

39

39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATATACATA TGGCTTACTC TCTGACTACG GGTTCGTGTTG TTATTGTTGG TAGAATTATT  
 TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA

60

96

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGTGGTGC TCGAGGCTGC CGCGCGGCAC CAGCGTAACG ACCTCCAGGT C

51

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GATATACATA TGGCTTACTC TCTGACTACG GGTTCGTGTTG TTATTGTTGG TAGAATTATT  
 TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA

60

96

(2) INFORMATION FOR SEQ ID NO:90:

Biotech : 222300

- (ii) MOLECULE TYPE: cDNA

- TGGTGGTGCT CGAGGCTGCC GCGCGGCACC AGCGTAACGA CCTCCAGGTC

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Asp Thr Glu Asp Val Val Ala Cys Ser Met Ser Tyr Thr Trp Tyr Gly  
1 5 10 15

Lys

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- ```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..651
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG  
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro

48

| 1                                                               | 5   | 10  | 15  |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA |     |     |     | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu | 20  | 25  | 30  |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA |     |     |     | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu | 35  | 40  | 45  |     |
| CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC |     |     |     | 192 |
| Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val | 50  | 55  | 60  |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG |     |     |     | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala | 65  | 70  | 75  | 80  |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA |     |     |     | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser | 85  | 90  | 95  |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT |     |     |     | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn | 100 | 105 | 110 |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC |     |     |     | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser | 115 | 120 | 125 |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA |     |     |     | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg | 130 | 135 | 140 |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC |     |     |     | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser | 145 | 150 | 155 | 160 |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT |     |     |     | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly | 165 | 170 | 175 |     |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC |     |     |     | 576 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala | 180 | 185 | 190 |     |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG |     |     |     | 624 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu | 195 | 200 | 205 |     |
| TCC ATG GAA ACT ACT ATG CGG TCT TGA                             |     |     |     | 651 |
| Ser Met Glu Thr Thr Met Arg Ser *                               | 210 | 215 |     |     |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG     | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |
| 130 135 140                                                     |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |
| 145 150 155 160                                                 |     |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly |     |
| 165 170 175                                                     |     |

CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576  
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
180 185 190

GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624  
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
195 200 205

TCC ATG GAA ACT ACT ATG CGG TCT TGA 651  
Ser Met Glu Thr Thr Met Arg Ser \*  
210 215

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15

CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
20 25 30

TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
35 40 45

CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
50 55 60

GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
65 70 75 80

ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
85 90 95

AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336  
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
100 105 110

GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384  
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
 115 120 125  
 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA 432  
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140  
 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC 480  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160  
 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT 528  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 TCC ATG GAA ACT ACT ATG CGG TCT TGA 651  
 Ser Met Glu Thr Thr Met Arg Ser \*  
 210 215

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35 40 45  
 CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
 Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 50 55 60  
 GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG 240  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 65 70 75 80  
 ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA 288  
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 85 90 95  
 AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT 336  
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 100 105 110  
 GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC 384  
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
 115 120 125  
 TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA 432  
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140  
 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC 480  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160  
 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT 528  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 TCC ATG GAA ACT ACT ATG CGG TCT TGA 651  
 Ser Met Glu Thr Thr Met Arg Ser \*  
 210 215

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 650 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |
| 130 135 140                                                     |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |
| 145 150 155 160                                                 |     |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly |     |
| 165 170 175                                                     |     |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC | 576 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |
| 180 185 190                                                     |     |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG | 624 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |

195

200

205

TCC ATG GAA ACT ACT ATG CGG TCT TG  
 Ser Met Glu Thr Thr Met Arg Ser  
 210 215

650

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG     | 48  |
| Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro     |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |

650 640 630 620 610 600 590 580 570 560 550 540 530 520 510 500 490 480 470 460 450 440 430 420 410 400 390 380 370 360 350 340 330 320 310 300 290 280 270 260 250 240 230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140  
 CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC 480  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160  
 CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT 528  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly  
 165 170 175  
 CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC 576  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG 624  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 TCC ATG GAA ACT ACT ATG CGG TCT TG 650  
 Ser Met Glu Thr Thr Met Arg Ser  
 210 215

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA 96  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA 144  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35 40 45  
 CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC 192  
 Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 50 55 60

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG<br>Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala<br>65 70 75 80     | 240 |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA<br>Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser<br>85 90 95        | 288 |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT<br>Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn<br>100 105 110     | 336 |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC<br>Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser<br>115 120 125     | 384 |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA<br>Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg<br>130 135 140     | 432 |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC<br>His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser<br>145 150 155 160 | 480 |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT<br>Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly<br>165 170 175     | 528 |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC<br>Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala<br>180 185 190     | 576 |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG<br>Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu<br>195 200 205     | 624 |
| TCC ATG GAA ACT ACT ATG CGG TCT TGA<br>Ser Met Glu Thr Thr Met Arg Ser *                                                                              | 651 |
| 210 215                                                                                                                                               |     |

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |
| 130 135 140                                                     |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |
| 145 150 155 160                                                 |     |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly |     |
| 165 170 175                                                     |     |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC | 576 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |
| 180 185 190                                                     |     |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG | 624 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |
| 195 200 205                                                     |     |
| TCC ATG GAA ACT ACT ATG CGG TCT TGA                             | 651 |
| Ser Met Glu Thr Thr Met Arg Ser *                               |     |
| 210 215                                                         |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..651
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|                   |            |                   |                   |                 |                   |                   |                   |                   |                  |                   |                  |                   |                   |                   |            |     |
|-------------------|------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|------------|-----|
| ATG<br>Met<br>1   | GGC<br>Gly | AGC<br>Ser        | AGC<br>Ser        | CAT<br>His<br>5 | CAT<br>His        | CAT<br>His        | CAT<br>His        | CAT<br>His        | CAC<br>His<br>10 | AGC<br>Ser        | AGC<br>Ser       | GGC<br>Gly        | CTG<br>Leu        | GTG<br>Val<br>15  | CCG<br>Pro | 48  |
| CGC<br>Arg        | GGC<br>Gly | AGC<br>Ser        | CAT<br>His<br>20  | ATG<br>Met      | GGT<br>Gly        | TCT<br>Ser        | GTT<br>Val        | GTT<br>Val        | ATT<br>Ile<br>25 | GTT<br>Val        | GGT<br>Gly       | AGA<br>Arg        | ATT<br>Ile<br>30  | ATT<br>Ile        | TTA<br>Leu | 96  |
| TCT<br>Ser        | CCT<br>Pro | GCT<br>Ala<br>35  | GGT<br>Gly        | GGT<br>Gly      | ATC<br>Ile        | ACG<br>Thr        | GCC<br>Ala<br>40  | TAC<br>Tyr        | TCC<br>Ser       | CAA<br>Gln        | CAG<br>Gln       | ACG<br>Thr<br>45  | CGG<br>Arg        | GGC<br>Gly        | CTA<br>Leu | 144 |
| CTT<br>Leu<br>50  | GGT<br>Gly | TGC<br>Cys        | ATC<br>Ile        | ATC<br>Ile      | ACT<br>Thr        | AGC<br>Ser<br>55  | CTT<br>Leu        | ACA<br>Thr        | GGC<br>Gly       | CGG<br>Arg        | GAC<br>Asp<br>60 | AAG<br>Lys        | AAC<br>Asn        | CAG<br>Gln        | GTC<br>Val | 192 |
| GAG<br>Glu<br>65  | GGA<br>Gly | GAG<br>Glu        | GTT<br>Val        | CAG<br>Gln      | GTG<br>Val<br>70  | GTT<br>Val        | TCC<br>Ser        | ACC<br>Thr        | GCA<br>Ala<br>75 | ACA<br>Thr        | CAA<br>Gln       | TCC<br>Ser        | TTC<br>Phe        | CTG<br>Leu<br>80  | GCG<br>Ala | 240 |
| ACC<br>Thr        | TGC<br>Cys | GTC<br>Val        | AAC<br>Asn<br>85  | GGC<br>Gly      | GTG<br>Val        | TGT<br>Cys        | TGG<br>Trp        | ACC<br>Thr        | GTT<br>Val<br>90 | TAC<br>Tyr        | CAT<br>His       | GGT<br>Gly        | GCT<br>Ala<br>95  | GGC<br>Gly        | TCA<br>Ser | 288 |
| AAG<br>Lys        | ACC<br>Thr | TTA<br>Leu        | GCC<br>Ala<br>100 | GGC<br>Gly      | CCA<br>Pro        | AAG<br>Lys        | GGG<br>Gly        | CCA<br>Pro<br>105 | ATC<br>Ile       | ACC<br>Thr        | CAG<br>Gln       | ATG<br>Met        | TAC<br>Tyr<br>110 | ACT<br>Thr        | AAT<br>Asn | 336 |
| GTG<br>Val        | GAC<br>Asp | CAG<br>Gln<br>115 | GAC<br>Asp        | CTC<br>Leu      | GTC<br>Val        | GGC<br>Gly        | TGG<br>Trp<br>120 | CAG<br>Gln        | GCG<br>Ala       | CCC<br>Pro        | CCC<br>Pro       | GGG<br>Gly<br>125 | GCG<br>Ala        | CGT<br>Arg        | TCC<br>Ser | 384 |
| TTG<br>Leu<br>130 | ACA<br>Thr | CCA<br>Pro        | TGC<br>Cys        | ACC<br>Thr      | TGT<br>Cys        | GGC<br>Gly<br>135 | AGC<br>Ser        | TCA<br>Ser        | GAC<br>Asp       | CTT<br>Leu<br>140 | TAC<br>Tyr       | TTG<br>Leu        | GTC<br>Val        | ACG<br>Thr        | AGA<br>Arg | 432 |
| CAT<br>His<br>145 | GCT<br>Ala | GAC<br>Asp        | GTC<br>Val        | ATT<br>Ile      | CCG<br>Pro<br>150 | GTG<br>Val        | CGC<br>Arg        | CGG<br>Arg        | CGG<br>Arg       | GGC<br>Gly<br>155 | GAC<br>Asp       | AGT<br>Ser        | AGG<br>Arg        | GGG<br>Gly<br>160 | AGC<br>Ser | 480 |

(2) INFORMATION FOR SEQ ID NO:101:

(A) LENGTH: 651 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101;

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GGC | AGC | AGC | CAT | CAT | CAT | CAT | CAC | AGC | AGC | GGC | CTG | GTG | CCG |     | 48  |
| Met | Gly | Ser | Ser | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |     |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| CGC | GGC | AGC | CAT | ATG | GGT | TCT | GTT | GTT | ATT | GTT | GGT | AGA | ATT | ATT | TTA | 96  |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| TCT | CCT | GCT | GGT | GGT | ATC | ACG | GCC | TAC | TCC | CAA | CAG | ACG | CGG | GGC | CTA | 144 |
| Ser | Pro | Ala | Gly | Gly | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| CTT | GGT | TGC | AAG | ATC | ACT | AGC | CTT | ACA | GGC | CGG | GAC | AAG | AAC | CAG | GTC | 192 |
| Leu | Gly | Cys | Lys | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| GAG | GGA | GAG | GTT | CAG | GTG | GTT | TCC | ACC | GCA | ACA | CAA | TCC | TTC | CTG | GCG | 240 |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| ACC | TGC | GTC | AAC | GGC | GTG | TGT | TGG | ACC | GTT | TAC | CAT | GGT | GCT | GGC | TCA | 288 |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser |     |

|                                                                 | 85  | 90  | 95  |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT |     |     |     | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |     |     |     |
|                                                                 | 100 | 105 | 110 |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC |     |     |     | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |     |     |     |
|                                                                 | 115 | 120 | 125 |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA |     |     |     | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |     |     |     |
|                                                                 | 130 | 135 | 140 |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC |     |     |     | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |     |     |     |
|                                                                 | 145 | 150 | 155 | 160 |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT |     |     |     | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly |     |     |     |     |
|                                                                 | 165 | 170 | 175 |     |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC |     |     |     | 576 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |     |     |     |
|                                                                 | 180 | 185 | 190 |     |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG |     |     |     | 624 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |     |     |     |
|                                                                 | 195 | 200 | 205 |     |
| TCC ATG GAA ACT ACT ATG CGG TCT TGA                             |     |     |     | 651 |
| Ser Met Glu Thr Thr Met Arg Ser *                               |     |     |     |     |
|                                                                 | 210 | 215 |     |     |

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48 |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |    |
| 1 5 10 15                                                       |    |



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |
| 130 135 140                                                     |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |
| 145 150 155 160                                                 |     |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly |     |
| 165 170 175                                                     |     |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC | 576 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |
| 180 185 190                                                     |     |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG | 624 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |
| 195 200 205                                                     |     |
| TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC | 672 |
| Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser |     |
| 210 215 220                                                     |     |
| CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC | 720 |
| Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro |     |
| 225 230 235 240                                                 |     |
| ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA | 768 |
| Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln |     |

| 245                                                                                                                                                   | 250 | 255 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG<br>Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly<br>260 265 270     |     |     | 816  |
| TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA<br>Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg<br>275 280 285     |     |     | 864  |
| ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC<br>Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr<br>290 295 300     |     |     | 912  |
| TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC<br>Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp<br>305 310 315 320 |     |     | 960  |
| ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG<br>Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu<br>325 330 335     |     |     | 1008 |
| GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT<br>Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu<br>340 345 350     |     |     | 1056 |
| GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC<br>Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His<br>355 360 365     |     |     | 1104 |
| CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC<br>Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe<br>370 375 380     |     |     | 1152 |
| TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC<br>Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu<br>385 390 395 400 |     |     | 1200 |
| ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG<br>Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu<br>405 410 415     |     |     | 1248 |
| TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG<br>Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val<br>420 425 430     |     |     | 1296 |
| TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT<br>Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala<br>435 440 445     |     |     | 1344 |
| CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC<br>Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn<br>450 455 460     |     |     | 1392 |
| ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC<br>Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr<br>465 470 475 480 |     |     | 1440 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ATT | GAG | ACG | ACG | ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | 1488 |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |      |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |
| CGG | GGT | AGG | ACT | GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | 1536 |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |
| CCG | GGA | GAA | CGG | CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | 1584 |
| Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu |      |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |
| TGC | TAT | GAC | GCG | GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | 1632 |
| Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr |      |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |      |
| TCG | GTT | AGG | TTG | CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | 1680 |
| Ser | Val | Arg | Leu | Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys |      |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |
| CAG | GAC | CAC | CTG | GAG | TTC | TGG | GAG | AGT | GTC | TTC | ACA | GGC | CTC | ACC | CAT | 1728 |
| Gln | Asp | His | Leu | Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His |      |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |      |
| ATA | GAT | GCA | CAC | TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | 1776 |
| Ile | Asp | Ala | His | Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe |      |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |
| CCC | TAC | CTG | GTA | GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | 1824 |
| Pro | Tyr | Leu | Val | Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala |      |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |      |
| CCA | CCT | CCA | TCA | TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | 1872 |
| Pro | Pro | Pro | Ser | Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys |      |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |
| CCT | ACG | CTG | CAC | GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | 1920 |
| Pro | Thr | Leu | His | Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val |      |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |
| CAA | AAT | GAG | GTC | ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA | 1968 |
| Gln | Asn | Glu | Val | Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala |      |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |      |
| TGC | ATG | TCG | GCT | GAC | CTG | GAG | GTC | GTC | ACT |     |     |     |     |     |     | 1998 |
| Cys | Met | Ser | Ala | Asp | Leu | Glu | Val | Val |     |     |     |     |     |     |     |      |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CCA | CTG | CTC | TGC | CCT | TCG | GGG | CAC | GCT | GTG | GGC | ATC | TTC | CGG | GCT | GCC | 576  |
| Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| GTA | TGC | ACC | CGG | GGG | GTT | GCG | AAG | GCG | GTG | GAC | TTT | GTG | CCC | GTA | GAG | 624  |
| Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val | Asp | Phe | Val | Pro | Val | Glu |      |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| TCC | ATG | GAA | ACT | ACT | ATG | CGG | TCT | CCG | GTC | TTC | ACG | GAC | AAC | TCA | TCC | 672  |
| Ser | Met | Glu | Thr | Thr | Met | Arg | Ser | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser |      |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| CCC | CCG | GCC | GTA | CCG | CAG | TCA | TTT | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC | 720  |
| Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro |      |
|     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| ACT | GGC | AGC | GGC | AAG | AGT | ACT | AAA | GTG | CCG | GCT | GCA | TAT | GCA | GCC | CAA | 768  |
| Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln |      |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |      |
| GGG | TAC | AAG | GTG | CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | 816  |
| Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly |      |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |      |
| TTT | GGG | GCG | TAT | ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | 864  |
| Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg |      |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | 912  |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr |      |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| TAT | GGC | AAG | TTT | CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | 960  |
| Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp |      |
|     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |      |
| ATC | ATA | ATA | TGT | GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | 1008 |
| Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| GGC | ATC | GGC | ACA | GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT | 1056 |
| Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu |      |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |      |
| GTC | GTG | CTC | GCC | ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | 1104 |
| Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His |      |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | 1152 |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |      |
|     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | 1200 |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |      |
|     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |     | 400 |      |
| ATT | TTC | TGT | CAT | TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | 1248 |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |      |

| 405                                                                                                                                                   | 410 | 415 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG<br>Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val<br>420 425 430     |     |     | 1296 |
| TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT<br>Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala<br>435 440 445     |     |     | 1344 |
| CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC<br>Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn<br>450 455 460     |     |     | 1392 |
| ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC<br>Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr<br>465 470 475 480 |     |     | 1440 |
| ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG.<br>Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg<br>485 490 495    |     |     | 1488 |
| CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT<br>Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr<br>500 505 510     |     |     | 1536 |
| CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG<br>Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu<br>515 520 525     |     |     | 1584 |
| TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC<br>Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr<br>530 535 540     |     |     | 1632 |
| TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC<br>Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys<br>545 550 555 560 |     |     | 1680 |
| CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT<br>Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His<br>565 570 575     |     |     | 1728 |
| ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC<br>Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe<br>580 585 590     |     |     | 1776 |
| CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC<br>Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala<br>595 600 605     |     |     | 1824 |
| CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA<br>Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys<br>610 615 620     |     |     | 1872 |
| CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC<br>Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val<br>625 630 635 640 |     |     | 1920 |

CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA 1968  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
                   645                                  650                                  655

TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998  
 Cys Met Ser Ala Asp Leu Glu Val Val  
                   660                                  665

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|                                                                                                                |     |
|----------------------------------------------------------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG                                                | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro                                                |     |
| 1                                  5                                  10                                  15   |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA                                                | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu                                                |     |
| 20                                  25                                  30                                     |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA                                                | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu                                                |     |
| 35                                  40                                  45                                     |     |
| CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC                                                | 192 |
| Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val                                                |     |
| 50                                  55                                  60                                     |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG                                                | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala                                                |     |
| 65                                  70                                  75                                  80 |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA                                                | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser                                                |     |
| 85                                  90                                  95                                     |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT                                                | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn                                                |     |
| 100                                  105                                  110                                  |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC                                                | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser                                                |     |

|                                                                 |     |     |      |
|-----------------------------------------------------------------|-----|-----|------|
| 115                                                             | 120 | 125 |      |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA |     |     | 432  |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |     |      |
| 130                                                             | 135 | 140 |      |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC |     |     | 480  |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |     |      |
| 145                                                             | 150 | 155 | 160  |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT |     |     | 528  |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly |     |     |      |
| 165                                                             | 170 | 175 |      |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC |     |     | 576  |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |     |      |
| 180                                                             | 185 | 190 |      |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG |     |     | 624  |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |     |      |
| 195                                                             | 200 | 205 |      |
| TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC |     |     | 672  |
| Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser |     |     |      |
| 210                                                             | 215 | 220 |      |
| CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC |     |     | 720  |
| Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro |     |     |      |
| 225                                                             | 230 | 235 | 240  |
| ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA |     |     | 768  |
| Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln |     |     |      |
| 245                                                             | 250 | 255 |      |
| GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG |     |     | 816  |
| Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly |     |     |      |
| 260                                                             | 265 | 270 |      |
| TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA |     |     | 864  |
| Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg |     |     |      |
| 275                                                             | 280 | 285 |      |
| ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC |     |     | 912  |
| Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr |     |     |      |
| 290                                                             | 295 | 300 |      |
| TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC |     |     | 960  |
| Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp |     |     |      |
| 305                                                             | 310 | 315 | 320  |
| ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG |     |     | 1008 |
| Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu |     |     |      |
| 325                                                             | 330 | 335 |      |
| GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT |     |     | 1056 |
| Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu |     |     |      |
| 340                                                             | 345 | 350 |      |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GTG | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | TCG | Val | ACC | GTG | CCA | CAC | 1104 |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | 1152 |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | 1200 |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATT | TTC | TGT | CAT | TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | 1248 |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| TCA | GGC | CTC | GGA | ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | 1296 |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TCC | GTC | ATA | CCA | ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | 1344 |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| CTG | ATG | ACG | GGC | TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | 1392 |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| ACA | TGT | GTC | ACC | CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | 1440 |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |
| ATT | GAG | ACG | ACG | ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | 1488 |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |      |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |
| CGG | GGT | AGG | ACT | GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | 1536 |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |
| CCG | GGA | GAA | CGG | CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | 1584 |
| Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu |      |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |
| TGC | TAT | GAC | GCG | GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | 1632 |
| Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr |      |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |      |
| TCG | GTT | AGG | TTG | CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | 1680 |
| Ser | Val | Arg | Leu | Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys |      |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |
| CAG | GAC | CAC | CTG | GAG | TTC | TGG | GAG | AGT | GTC | TTC | ACA | GGC | CTC | ACC | CAT | 1728 |
| Gln | Asp | His | Leu | Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His |      |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     | 575 |     |     |      |
| ATA | GAT | GCA | CAC | TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | 1776 |
| Ile | Asp | Ala | His | Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe |      |

| 580 |     |     |     |     |     |     |     |     |     | 585 |     |     |     |     | 590 |  |      |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|--|--|--|
| CCC | TAC | CTG | GTA | GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC |  | 1824 |  |  |  |
| Pro | Tyr | Leu | Val | Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala |  |      |  |  |  |
|     |     | 595 |     |     |     |     |     | 600 |     |     |     | 605 |     |     |     |  |      |  |  |  |
| CCA | CCT | CCA | TCA | TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA |  | 1872 |  |  |  |
| Pro | Pro | Pro | Ser | Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys |  |      |  |  |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |      |  |  |  |
| CCT | ACG | CTG | CAC | GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC |  | 1920 |  |  |  |
| Pro | Thr | Leu | His | Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val |  |      |  |  |  |
|     | 625 |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |      |  |  |  |
| CAA | AAT | GAG | GTC | ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA |  | 1968 |  |  |  |
| Gln | Asn | Glu | Val | Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala |  |      |  |  |  |
|     |     |     | 645 |     |     |     |     |     | 650 |     |     |     |     |     | 655 |  |      |  |  |  |
| TGC | ATG | TCG | GCT | GAC | CTG | GAG | GTC | GTC | ACT |     |     |     |     |     |     |  | 1998 |  |  |  |
| Cys | Met | Ser | Ala | Asp | Leu | Glu | Val | Val |     |     |     |     |     |     |     |  |      |  |  |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     |     |     |     |  |      |  |  |  |

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| ATG | GGC | AGC | AGC | CAT | CAT | CAT | CAT | CAT | CAC | AGC | AGC | GGC | CTG | GTG | CCG |  | 48  |
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |  |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |     |
| CGC | GGC | AGC | CAT | ATG | GGT | TCT | GTT | GTT | ATT | GTT | GGT | AGA | ATT | ATT | TTA |  | 96  |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |  |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |     |
| TCT | GGT | AGT | GGT | AGT | ATC | ACG | GCC | TAC | TCC | CAA | CAG | ACG | CGG | GGC | CTA |  | 144 |
| Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |  |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |     |
| CTT | GGT | TGC | AAG | AAG | ACT | AGC | CTT | ACA | GGC | CGG | GAC | AAG | AAC | CAG | GTC |  | 192 |
| Leu | Gly | Cys | Lys | Lys | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val |  |     |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAG | GGA | GAG | GTT | CAG | GTG | GTT | TCC | ACC | GCA | ACA | CAA | TCC | TTC | CTG | GCG | 240 |
| Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| ACC | TGC | GTC | AAC | GGC | GTG | TGT | TGG | ACC | GTT | TAC | CAT | GGT | GCT | GGC | TCA | 288 |
| Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| AAG | ACC | TTA | GCC | GGC | CCA | AAG | GGG | CCA | ATC | ACC | CAG | ATG | TAC | ACT | AAT | 336 |
| Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTG | GAC | CAG | GAC | CTC | GTC | GGC | TGG | CAG | GCG | CCC | CCC | GGG | GCG | CGT | TCC | 384 |
| Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| TTG | ACA | CCA | TGC | ACC | TGT | GGC | AGC | TCA | GAC | CTT | TAC | TTG | GTC | ACG | AGA | 432 |
| Leu | Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| CAT | GCT | GAC | GTC | ATT | CCG | GTG | CGC | CGG | CGG | GGC | GAC | AGT | AGG | GGG | AGC | 480 |
| His | Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| CTG | CTC | TCC | CCC | AGG | CCT | GTC | TCC | TAC | TTG | AAG | GGC | TCT | TCG | GGT | GGT | 528 |
| Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ser | Gly | Gly |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| CCA | CTG | CTC | TGC | CCT | TCG | GGG | CAC | GCT | GTG | GGC | ATC | TTC | CGG | GCT | GCC | 576 |
| Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| GTA | TGC | ACC | CGG | GGG | GTT | GCG | AAG | GCG | GTG | GAC | TTT | GTG | CCC | GTA | GAG | 624 |
| Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val | Asp | Phe | Val | Pro | Val | Glu |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| TCC | ATG | GAA | ACT | ACT | ATG | CGG | TCT | CCG | GTC | TTC | ACG | GAC | AAC | TCA | TCC | 672 |
| Ser | Met | Glu | Thr | Thr | Met | Arg | Ser | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| CCC | CCG | GCC | GTA | CCG | CAG | TCA | TTT | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC | 720 |
| Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| ACT | GGC | AGC | GGC | AAG | AGT | ACT | AAA | GTG | CCG | GCT | GCA | TAT | GCA | GCC | CAA | 768 |
| Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| GGG | TAC | AAG | GTG | CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | 816 |
| Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| TTT | GGG | GCG | TAT | ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | 864 |
| Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | 912 |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr |     |

| 290                                                                                                                                                   | 295 | 300 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC<br>Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp<br>305 310 315 320 |     |     | 960  |
| ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG<br>Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu<br>325 330 335     |     |     | 1008 |
| GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT<br>Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu<br>340 345 350     |     |     | 1056 |
| GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC<br>Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His<br>355 360 365     |     |     | 1104 |
| CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC<br>Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe<br>370 375 380     |     |     | 1152 |
| TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC<br>Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu<br>385 390 395 400 |     |     | 1200 |
| ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG<br>Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu<br>405 410 415     |     |     | 1248 |
| TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG<br>Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val<br>420 425 430     |     |     | 1296 |
| TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT<br>Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala<br>435 440 445     |     |     | 1344 |
| CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC<br>Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn<br>450 455 460     |     |     | 1392 |
| ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC<br>Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr<br>465 470 475 480 |     |     | 1440 |
| ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG<br>Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg<br>485 490 495     |     |     | 1488 |
| CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT<br>Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr<br>500 505 510     |     |     | 1536 |
| CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG<br>Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu<br>515 520 525     |     |     | 1584 |

TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC 1632  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540

TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC 1680  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560

CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT 1728  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575

ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC 1776  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590

CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC 1824  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605

CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA 1872  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620

CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC 1920  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640

CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA 1968  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655

TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998  
 Cys Met Ser Ala Asp Leu Glu Val Val  
 660 665

## (2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1998 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48  
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |
| 130 135 140                                                     |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |
| 145 150 155 160                                                 |     |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly |     |
| 165 170 175                                                     |     |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC | 576 |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |     |
| 180 185 190                                                     |     |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG | 624 |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |     |
| 195 200 205                                                     |     |
| TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC | 672 |
| Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser |     |
| 210 215 220                                                     |     |
| CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC | 720 |
| Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro |     |
| 225 230 235 240                                                 |     |
| ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA | 768 |

| Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln |      |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|
| 245 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 250  | 255 |     |
| GGG | TAC | AAG | GTG | CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | 816  |     |     |
| Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly |      |     |     |
| 260 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 265  | 270 |     |
| TTT | GGG | GCG | TAT | ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | 864  |     |     |
| Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg |      |     |     |
| 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 280  | 285 |     |
| ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | 912  |     |     |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr |      |     |     |
| 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 295  | 300 |     |
| TAT | GGC | AAG | TTT | CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | 960  |     |     |
| Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp |      |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 310  | 315 | 320 |
| ATC | ATA | ATA | TGT | GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | 1008 |     |     |
| Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu |      |     |     |
| 325 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 330  | 335 |     |
| GGC | ATC | GGC | ACA | GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT | 1056 |     |     |
| Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu |      |     |     |
| 340 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 345  | 350 |     |
| GTC | GTG | CTC | GCC | ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | 1104 |     |     |
| Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His |      |     |     |
| 355 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 360  | 365 |     |
| CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | 1152 |     |     |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |      |     |     |
| 370 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 375  | 380 |     |
| TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | 1200 |     |     |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |      |     |     |
| 385 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 390  | 395 | 400 |
| ATT | TTC | TGT | CAT | TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | 1248 |     |     |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |      |     |     |
| 405 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 410  | 415 |     |
| TCA | GGC | CTC | GGA | ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | 1296 |     |     |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |      |     |     |
| 420 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 425  | 430 |     |
| TCC | GTC | ATA | CCA | ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | 1344 |     |     |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |      |     |     |
| 435 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 440  | 445 |     |
| CTG | ATG | ACG | GGC | TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | 1392 |     |     |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |      |     |     |
| 450 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 455  | 460 |     |
| ACA | TGT | GTC | ACC | CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | 1440 |     |     |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |      |     |     |
| 465 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 470  | 475 | 480 |

|                                                                                                                                    |      |
|------------------------------------------------------------------------------------------------------------------------------------|------|
| ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG<br>Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg | 1488 |
| 485 490 495                                                                                                                        |      |
| CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT<br>Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr | 1536 |
| 500 505 510                                                                                                                        |      |
| CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG<br>Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu | 1584 |
| 515 520 525                                                                                                                        |      |
| TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC<br>Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr | 1632 |
| 530 535 540                                                                                                                        |      |
| TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC<br>Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys | 1680 |
| 545 550 555 560                                                                                                                    |      |
| CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT<br>Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His | 1728 |
| 565 570 575                                                                                                                        |      |
| ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC<br>Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe | 1776 |
| 580 585 590                                                                                                                        |      |
| CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC<br>Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala | 1824 |
| 595 600 605                                                                                                                        |      |
| CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA<br>Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys | 1872 |
| 610 615 620                                                                                                                        |      |
| CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC<br>Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val | 1920 |
| 625 630 635 640                                                                                                                    |      |
| CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA<br>Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala | 1968 |
| 645 650 655                                                                                                                        |      |
| TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT<br>Cys Met Ser Ala Asp Leu Glu Val Val                                                     | 1998 |
| 660 665                                                                                                                            |      |

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1997

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu |     |
| 35 40 45                                                        |     |
| CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC | 192 |
| Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val |     |
| 50 55 60                                                        |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala |     |
| 65 70 75 80                                                     |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser |     |
| 85 90 95                                                        |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn |     |
| 100 105 110                                                     |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC | 384 |
| Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser |     |
| 115 120 125                                                     |     |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA | 432 |
| Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg |     |
| 130 135 140                                                     |     |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC | 480 |
| His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser |     |
| 145 150 155 160                                                 |     |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT | 528 |
| Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly |     |
| 165 170 175                                                     |     |

Biotech = 62436150

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC | 576  |
| Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala |      |
| 180 185 190                                                     |      |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG | 624  |
| Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu |      |
| 195 200 205                                                     |      |
| TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC | 672  |
| Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser |      |
| 210 215 220                                                     |      |
| CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC | 720  |
| Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro |      |
| 225 230 235 240                                                 |      |
| ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA | 768  |
| Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln |      |
| 245 250 255                                                     |      |
| GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG | 816  |
| Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly |      |
| 260 265 270                                                     |      |
| TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA | 864  |
| Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg |      |
| 275 280 285                                                     |      |
| ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC | 912  |
| Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr |      |
| 290 295 300                                                     |      |
| TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC | 960  |
| Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp |      |
| 305 310 315 320                                                 |      |
| ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG | 1008 |
| Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu |      |
| 325 330 335                                                     |      |
| GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT | 1056 |
| Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu |      |
| 340 345 350                                                     |      |
| GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC | 1104 |
| Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His |      |
| 355 360 365                                                     |      |
| CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC | 1152 |
| Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe |      |
| 370 375 380                                                     |      |
| TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC | 1200 |
| Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu |      |
| 385 390 395 400                                                 |      |
| ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG | 1248 |
| Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|
| 405 |     |     |     |     |     |     |     |     |     | 410 |     |     |     |     | 415 |      |  |  |  |  |
| TCA | GGC | CTC | GGA | ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | 1296 |  |  |  |  |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |      |  |  |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |  |  |  |  |
| TCC | GTC | ATA | CCA | ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | 1344 |  |  |  |  |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |      |  |  |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |  |  |  |  |
| CTG | ATG | ACG | GGC | TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | 1392 |  |  |  |  |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |      |  |  |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |  |  |  |  |
| ACA | TGT | GTC | ACC | CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | 1440 |  |  |  |  |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |      |  |  |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |  |  |  |  |
| ATT | GAG | ACG | ACG | ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | 1488 |  |  |  |  |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |      |  |  |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |  |  |  |  |
| CGG | GGT | AGG | ACT | GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | 1536 |  |  |  |  |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |      |  |  |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |  |  |  |  |
| CCG | GGA | GAA | CGG | CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | 1584 |  |  |  |  |
| Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu |      |  |  |  |  |
|     |     | 515 |     |     |     | 520 |     |     |     |     |     | 525 |     |     |     |      |  |  |  |  |
| TGC | TAT | GAC | GCG | GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | 1632 |  |  |  |  |
| Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr |      |  |  |  |  |
|     | 530 |     |     |     | 535 |     |     |     |     |     | 540 |     |     |     |     |      |  |  |  |  |
| TCG | GTT | AGG | TTG | CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | 1680 |  |  |  |  |
| Ser | Val | Arg | Leu | Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys |      |  |  |  |  |
| 545 |     |     |     | 550 |     |     |     | 555 |     |     |     |     |     |     | 560 |      |  |  |  |  |
| CAG | GAC | CAC | CTG | GAG | TTC | TGG | GAG | AGT | GTC | TTC | ACA | GGC | CTC | ACC | CAT | 1728 |  |  |  |  |
| Gln | Asp | His | Leu | Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His |      |  |  |  |  |
|     |     |     |     | 565 |     |     |     | 570 |     |     |     |     |     | 575 |     |      |  |  |  |  |
| ATA | GAT | GCA | CAC | TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | 1776 |  |  |  |  |
| Ile | Asp | Ala | His | Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe |      |  |  |  |  |
|     |     |     | 580 |     |     |     | 585 |     |     |     |     |     | 590 |     |     |      |  |  |  |  |
| CCC | TAC | CTG | GTA | GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | 1824 |  |  |  |  |
| Pro | Tyr | Leu | Val | Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala |      |  |  |  |  |
|     |     | 595 |     |     |     | 600 |     |     |     |     |     | 605 |     |     |     |      |  |  |  |  |
| CCA | CCT | CCA | TCA | TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | 1872 |  |  |  |  |
| Pro | Pro | Pro | Ser | Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys |      |  |  |  |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |  |  |  |  |
| CCT | ACG | CTG | CAC | GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | 1920 |  |  |  |  |
| Pro | Thr | Leu | His | Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val |      |  |  |  |  |
| 625 |     |     |     | 630 |     |     |     | 635 |     |     |     |     |     |     | 640 |      |  |  |  |  |

CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA 1968  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
                   645                                  650                                  655

TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT 1998  
 Cys Met Ser Ala Asp Leu Glu Val Val  
                   660                                  665

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

|                                                                                                                |     |
|----------------------------------------------------------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG                                                | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro                                                |     |
| 1                                  5                                  10                                  15   |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA                                                | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu                                                |     |
| 20                                  25                                  30                                     |     |
| TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA                                                | 144 |
| Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu                                                |     |
| 35                                  40                                  45                                     |     |
| CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC                                                | 192 |
| Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val                                                |     |
| 50                                  55                                  60                                     |     |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG                                                | 240 |
| Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala                                                |     |
| 65                                  70                                  75                                  80 |     |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA                                                | 288 |
| Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser                                                |     |
| 85                                  90                                  95                                     |     |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT                                                | 336 |
| Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn                                                |     |
| 100                                  105                                  110                                  |     |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC                                                | 384 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser |  |      |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |      |
| TTG | ACA | CCA | TGC | ACC | TGT | GGC | AGC | TCA | GAC | CTT | TAC | TTG | GTC | ACG | AGA |  | 432  |
| Leu | Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg |  |      |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |      |
| CAT | GCT | GAC | GTC | ATT | CCG | GTG | CGC | CGG | CGG | GGC | GAC | AGT | AGG | GGG | AGC |  | 480  |
| His | Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser |  |      |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |      |
| CTG | CTC | TCC | CCC | AGG | CCT | GTC | TCC | TAC | TTG | AAG | GGC | TCT | GCT | GGT | GGT |  | 528  |
| Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ala | Gly | Gly |  |      |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |      |
| CCA | CTG | CTC | TGC | CCT | TCG | GGG | CAC | GCT | GTG | GGC | ATC | TTC | CGG | GCT | GCC |  | 576  |
| Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala |  |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |      |
| GTA | TGC | ACC | CGG | GGG | GTT | GCG | AAG | GCG | GTG | GAC | TTT | GTG | CCC | GTA | GAG |  | 624  |
| Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val | Asp | Phe | Val | Pro | Val | Glu |  |      |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |      |
| TCC | ATG | GAA | ACT | ACT | ATG | CGG | TCT | CCG | GTC | TTC | ACG | GAC | AAC | TCA | TCC |  | 672  |
| Ser | Met | Glu | Thr | Thr | Met | Arg | Ser | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser |  |      |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |      |
| CCC | CCG | GCC | GTA | CCG | CAG | TCA | TTT | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC |  | 720  |
| Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro |  |      |
|     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |      |
| ACT | GGC | AGC | GGC | AAG | AGT | ACT | AAA | GTG | CCG | GCT | GCA | TAT | GCA | GCC | CAA |  | 768  |
| Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln |  |      |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |  |      |
| GGG | TAC | AAG | GTG | CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG |  | 816  |
| Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly |  |      |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |      |
| TTT | GGG | GCG | TAT | ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA |  | 864  |
| Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg |  |      |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |  |      |
| ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC |  | 912  |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr |  |      |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |      |
| TAT | GGC | AAG | TTT | CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC |  | 960  |
| Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp |  |      |
|     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |     |  |      |
| ATC | ATA | ATA | TGT | GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG |  | 1008 |
| Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu |  |      |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |  |      |
| GGC | ATC | GGC | ACA | GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT |  | 1056 |
| Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu |  |      |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |  |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GTC | GTG | CTC | GCC | ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | 1104 |
| Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | 1152 |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | 1200 |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATT | TTC | TGT | CAT | TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | 1248 |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| TCA | GGC | CTC | GGA | ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | 1296 |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |      |
| TCC | GTC | ATA | CCA | ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | 1344 |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |      |
| CTG | ATG | ACG | GGC | TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | 1392 |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| ACA | TGT | GTC | ACC | CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | 1440 |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |
| ATT | GAG | ACG | ACG | ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | 1488 |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |      |
|     |     |     |     | 485 |     |     |     | 490 |     |     |     |     |     | 495 |     |      |
| CGG | GGT | AGG | ACT | GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | 1536 |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |      |
|     |     |     | 500 |     |     |     | 505 |     |     |     |     |     |     | 510 |     |      |
| CCG | GGA | GAA | CGG | CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | 1584 |
| Pro | Gly | Glu | Arg | Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu |      |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |
| TGC | TAT | GAC | GCG | GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | 1632 |
| Cys | Tyr | Asp | Ala | Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr |      |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |      |
| TCG | GTT | AGG | TTG | CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | 1680 |
| Ser | Val | Arg | Leu | Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys |      |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |
| CAG | GAC | CAC | CTG | GAG | TTC | TGG | GAG | AGT | GTC | TTC | ACA | GGC | CTC | ACC | CAT | 1728 |
| Gln | Asp | His | Leu | Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His |      |
|     |     |     |     | 565 |     |     |     | 570 |     |     |     |     |     | 575 |     |      |
| ATA | GAT | GCA | CAC | TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | 1776 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ile | Asp | Ala | His | Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe |      |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |  |
| CCC | TAC | CTG | GTA | GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | 1824 |  |
| Pro | Tyr | Leu | Val | Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala |      |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |      |  |
| CCA | CCT | CCA | TCA | TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | 1872 |  |
| Pro | Pro | Pro | Ser | Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys |      |  |
|     | 610 |     |     |     |     |     | 615 |     |     |     | 620 |     |     |     |     |      |  |
| CCT | ACG | CTG | CAC | GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | 1920 |  |
| Pro | Thr | Leu | His | Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val |      |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |  |
| CAA | AAT | GAG | GTC | ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA | 1968 |  |
| Gln | Asn | Glu | Val | Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala |      |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |      |  |
| TGC | ATG | TCG | GCT | GAC | CTG | GAG | GTC | GTC | ACT |     |     |     |     |     |     | 1998 |  |
| Cys | Met | Ser | Ala | Asp | Leu | Glu | Val | Val |     |     |     |     |     |     |     |      |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1997

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1995

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| ATG | GGC | AGC | AGC | CAT | CAT | CAT | CAT | CAT | CAC | AGC | AGC | GGC | CTG | GTG | CCG | 48  |  |
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |     |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| CGC | GGC | AGC | CAT | ATG | GGT | TCT | GTT | GTT | ATT | GTT | GGT | AGA | ATT | ATT | TTA | 96  |  |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |     |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| TCT | GGT | AGT | GGT | AGT | ATC | ACG | GCC | TAC | TCC | CAA | CAG | ACG | CGG | GGC | CTA | 144 |  |
| Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu |     |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC<br>Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val<br>50 55 60        | 192 |
| GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG<br>Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala<br>65 70 75 80     | 240 |
| ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA<br>Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser<br>85 90 95        | 288 |
| AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT<br>Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn<br>100 105 110     | 336 |
| GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC<br>Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser<br>115 120 125     | 384 |
| TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA<br>Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg<br>130 135 140     | 432 |
| CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC<br>His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser<br>145 150 155 160 | 480 |
| CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT<br>Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly<br>165 170 175     | 528 |
| CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC<br>Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala<br>180 185 190     | 576 |
| GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG<br>Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu<br>195 200 205     | 624 |
| TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC<br>Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser<br>210 215 220     | 672 |
| CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC<br>Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro<br>225 230 235 240 | 720 |
| ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG GCT GCA TAT GCA GCC CAA<br>Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln<br>245 250 255     | 768 |
| GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC GTT GCC GCT ACC TTA GGG<br>Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly<br>260 265 270     | 816 |
| TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT ATT GAC CCC AAC ATC AGA<br>Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg                    | 864 |



| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | 912  |
| Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| TAT | GGC | AAG | TTT | CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | 960  |
| Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp |      |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |      |
| ATC | ATA | ATA | TGT | GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | 1008 |
| Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| GGC | ATC | GGC | ACA | GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT | 1056 |
| Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| GTC | GTG | CTC | GCC | ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | 1104 |
| Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | 1152 |
| Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | 1200 |
| Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATT | TTC | TGT | CAT | TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | 1248 |
| Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| TCA | GGC | CTC | GGA | ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | 1296 |
| Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TCC | GTC | ATA | CCA | ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | 1344 |
| Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| CTG | ATG | ACG | GGC | TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | 1392 |
| Leu | Met | Thr | Gly | Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| ACA | TGT | GTC | ACC | CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | 1440 |
| Thr | Cys | Val | Thr | Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |
| ATT | GAG | ACG | ACG | ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | 1488 |
| Ile | Glu | Thr | Thr | Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg |      |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |
| CGG | GGT | AGG | ACT | GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | 1536 |
| Arg | Gly | Arg | Thr | Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG | 1584 |
| Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu |      |
| 515 520 525                                                     |      |
| TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC | 1632 |
| Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr |      |
| 530 535 540                                                     |      |
| TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC | 1680 |
| Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys |      |
| 545 550 555 560                                                 |      |
| CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT | 1728 |
| Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His |      |
| 565 570 575                                                     |      |
| ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC | 1776 |
| Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe |      |
| 580 585 590                                                     |      |
| CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC | 1824 |
| Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala |      |
| 595 600 605                                                     |      |
| CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA | 1872 |
| Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys |      |
| 610 615 620                                                     |      |
| CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC | 1920 |
| Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val |      |
| 625 630 635 640                                                 |      |
| CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA | 1968 |
| Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala |      |
| 645 650 655                                                     |      |
| TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT                         | 1998 |
| Cys Met Ser Ala Asp Leu Glu Val Val                             |      |
| 660 665                                                         |      |

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2013

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GGC | AGC | AGC | CAT | CAT | CAT | CAT | CAT | CAC | AGC | AGC | GGC | CTG | GTG | CCG | 48  |
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CGC | GGC | AGC | CAT | ATG | GCT | TAC | TCT | CTG | ACT | ACG | GGT | TCT | GTT | GTT | ATT | 96  |
| Arg | Gly | Ser | His | Met | Ala | Tyr | Ser | Leu | Thr | Thr | Gly | Ser | Val | Val | Ile |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GTT | GGT | AGA | ATT | ATT | TTA | TCT | GGT | AGT | GGT | AGT | ATC | ACG | GCC | TAC | TCC | 144 |
| Val | Gly | Arg | Ile | Ile | Leu | Ser | Gly | Ser | Gly | Ser | Ile | Thr | Ala | Tyr | Ser |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| CAA | CAG | ACG | CGG | GGC | CTA | CTT | GGT | TGC | ATC | ATC | ACT | AGC | CTT | ACA | GGC | 192 |
| Gln | Gln | Thr | Arg | Gly | Leu | Leu | Gly | Cys | Ile | Ile | Thr | Ser | Leu | Thr | Gly |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CGG | GAC | AAG | AAC | CAG | GTC | GAG | GGA | GAG | GTT | CAG | GTG | GTT | TCC | ACC | GCA | 240 |
| Arg | Asp | Lys | Asn | Gln | Val | Glu | Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| ACA | CAA | TCC | TTC | CTG | GCG | ACC | TGC | GTC | AAC | GGC | GTG | TGT | TGG | ACC | GTT | 288 |
| Thr | Gln | Ser | Phe | Leu | Ala | Thr | Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAC | CAT | GGT | GCT | GGC | TCA | AAG | ACC | TTA | GCC | GGC | CCA | AAG | GGG | CCA | ATC | 336 |
| Tyr | His | Gly | Ala | Gly | Ser | Lys | Thr | Leu | Ala | Gly | Pro | Lys | Gly | Pro | Ile |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| ACC | CAG | ATG | TAC | ACT | AAT | GTG | GAC | CAG | GAC | CTC | GTC | GGC | TGG | CAG | GCG | 384 |
| Thr | Gln | Met | Tyr | Thr | Asn | Val | Asp | Gln | Asp | Leu | Val | Gly | Trp | Gln | Ala |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| CCC | CCC | GGG | GCG | CGT | TCC | TTG | ACA | CCA | TGC | ACC | TGT | GGC | AGC | TCA | GAC | 432 |
| Pro | Pro | Gly | Ala | Arg | Ser | Leu | Thr | Pro | Cys | Thr | Cys | Gly | Ser | Ser | Asp |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| CTT | TAC | TTG | GTC | ACG | AGA | CAT | GCT | GAC | GTC | ATT | CCG | GTG | CGC | CGG | CGG | 480 |
| Leu | Tyr | Leu | Val | Thr | Arg | His | Ala | Asp | Val | Ile | Pro | Val | Arg | Arg | Arg |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| GGC | GAC | AGT | AGG | GGG | AGC | CTG | CTC | TCC | CCC | AGG | CCT | GTC | TCC | TAC | TTG | 528 |
| Gly | Asp | Ser | Arg | Gly | Ser | Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| AAG | GGC | TCT | TCG | GGT | GGT | CCA | CTG | CTC | TGC | CCT | TCG | GGG | CAC | GCT | GTG | 576 |
| Lys | Gly | Ser | Ser | Gly | Gly | Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| GGC | ATC | TTC | CGG | GCT | GCC | GTA | TGC | ACC | CGG | GGG | GTT | GCG | AAG | GCG | GTG | 624 |
| Gly | Ile | Phe | Arg | Ala | Ala | Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val |     |
|     |     | 195 |     |     |     |     | 200 |     |     | </  |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TTC | ACG | GAC | AAC | TCA | TCC | CCC | CCG | GCC | GTA | CCG | CAG | TCA | TTT | CAA | GTG | 720  |
| Phe | Thr | Asp | Asn | Ser | Ser | Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| GCC | CAC | CTA | CAC | GCT | CCC | ACT | GGC | AGC | GGC | AAG | AGT | ACT | AAA | GTG | CCG | 768  |
| Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| GCT | GCA | TAT | GCA | GCC | CAA | GGG | TAC | AAG | GTG | CTC | GTC | CTC | AAT | CCG | TCC | 816  |
| Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| GTT | GCC | GCT | ACC | TTA | GGG | TTT | GGG | GCG | TAT | ATG | TCT | AAG | GCA | CAC | GGT | 864  |
| Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | 912  |
| Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | CTT | GCC | GAT | GGT | GGT | TGC | 960  |
| Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | GAT | GAG | TGC | CAT | TCA | ACT | 1008 |
| Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| GAC | TCG | ACT | ACA | ATC | TTG | GGC | ATC | GGC | ACA | GTC | CTG | GAC | CAA | GCG | GAG | 1056 |
| Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| ACG | GCT | GGA | GCG | CGG | CTT | GTC | GTG | CTC | GCC | ACC | GCT | ACG | CCT | CCG | GGA | 1104 |
| Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly |      |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |      |
| TCG | GTC | ACC | GTG | CCA | CAC | CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | 1152 |
| Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| ACT | GGA | GAG | ATC | CCC | TTC | TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | 1200 |
| Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala | Ile | Pro | Ile | Glu | Ala | Ile |      |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     | 400 |      |
| AGG | GGG | GGA | AGG | CAT | CTC | ATT | TTC | TGT | CAT | TCC | AAG | AAG | AAG | TGC | GAC | 1248 |
| Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His | Ser | Lys | Lys | Lys | Cys | Asp |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| GAG | CTC | GCC | GCA | AAG | CTG | TCA | GGC | CTC | GGA | ATC | AAC | GCT | GTG | GCG | TAT | 1296 |
| Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly | Ile | Asn | Ala | Val | Ala | Tyr |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TAC | CGG | GGG | CTC | GAT | GTG | TCC | GTC | ATA | CCA | ACT | ATC | GGA | GAC | GTC | GTT | 1344 |
| Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro | Thr | Ile | Gly | Asp | Val | Val |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| GTC | GTG | GCA | ACA | GAC | GCT | CTG | ATG | ACG | GGC | TAT | ACG | GGC | GAC | TTT | GAC | 1392 |

ACT

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2013

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT GTT ATT | 96  |
| Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile |     |
| 20 25 30                                                        |     |
| GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC | 144 |
| Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser |     |
| 35 40 45                                                        |     |
| CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC | 192 |
| Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly |     |
| 50 55 60                                                        |     |
| CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA | 240 |
| Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala |     |
| 65 70 75 80                                                     |     |
| ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT | 288 |
| Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val |     |
| 85 90 95                                                        |     |
| TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC | 336 |
| Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile |     |
| 100 105 110                                                     |     |
| ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG | 384 |
| Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln Ala |     |
| 115 120 125                                                     |     |
| CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC | 432 |
| Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp |     |
| 130 135 140                                                     |     |
| CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG | 480 |
| Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg Arg |     |
| 145 150 155 160                                                 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GGC | GAC | AGT | AGG | GGG | AGC | CTG | CTC | TCC | CCC | AGG | CCT | GTC | TCC | TAC | TTG | 528  |
| Gly | Asp | Ser | Arg | Gly | Ser | Leu | Leu | Ser | Pro | Arg | Pro | Val | Ser | Tyr | Leu |      |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |
| AAG | GGC | TCT | GCT | GGT | GGT | CCA | CTG | CTC | TGC | CCT | TCG | GGG | CAC | GCT | GTG | 576  |
| Lys | Gly | Ser | Ala | Gly | Gly | Pro | Leu | Leu | Cys | Pro | Ser | Gly | His | Ala | Val |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| GGC | ATC | TTC | CGG | GCT | GCC | GTA | TGC | ACC | CGG | GGG | GTT | GCG | AAG | GCG | GTG | 624  |
| Gly | Ile | Phe | Arg | Ala | Ala | Val | Cys | Thr | Arg | Gly | Val | Ala | Lys | Ala | Val |      |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| GAC | TTT | GTG | CCC | GTA | GAG | TCC | ATG | GAA | ACT | ACT | ATG | CGG | TCT | CCG | GTC | 672  |
| Asp | Phe | Val | Pro | Val | Glu | Ser | Met | Glu | Thr | Thr | Met | Arg | Ser | Pro | Val |      |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| TTC | ACG | GAC | AAC | TCA | TCC | CCC | CCG | GCC | GTA | CCG | CAG | TCA | TTT | CAA | GTG | 720  |
| Phe | Thr | Asp | Asn | Ser | Ser | Pro | Pro | Ala | Val | Pro | Gln | Ser | Phe | Gln | Val |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| GCC | CAC | CTA | CAC | GCT | CCC | ACT | GGC | AGC | GGC | AAG | AGT | ACT | AAA | GTG | CCG | 768  |
| Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly | Lys | Ser | Thr | Lys | Val | Pro |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| GCT | GCA | TAT | GCA | GCC | CAA | GGG | TAC | AAG | GTG | CTC | GTC | CTC | AAT | CCG | TCC | 816  |
| Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Pro | Ser |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| GTT | GCC | GCT | ACC | TTA | GGG | TTT | GGG | GCG | TAT | ATG | TCT | AAG | GCA | CAC | GGT | 864  |
| Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr | Met | Ser | Lys | Ala | His | Gly |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | ACC | ATT | ACC | ACA | GGC | GCC | 912  |
| Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg | Thr | Ile | Thr | Thr | Gly | Ala |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | CTT | GCC | GAT | GGT | GGT | TGC | 960  |
| Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe | Leu | Ala | Asp | Gly | Gly | Cys |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | GAT | GAG | TGC | CAT | TCA | ACT | 1008 |
| Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys | Asp | Glu | Cys | His | Ser | Thr |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| GAC | TCG | ACT | ACA | ATC | TTG | GGC | ATC | GGC | ACA | GTC | CTG | GAC | CAA | GCG | GAG | 1056 |
| Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr | Val | Leu | Asp | Gln | Ala | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| ACG | GCT | GGA | GCG | CGG | CTT | GTC | GTG | CTC | GCC | ACC | GCT | ACG | CCT | CCG | GGA | 1104 |
| Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala | Thr | Ala | Thr | Pro | Pro | Gly |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| TCG | GTC | ACC | GTG | CCA | CAC | CCA | AAC | ATC | GAG | GAG | GTG | GCC | CTG | TCT | AAT | 1152 |
| Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu | Glu | Val | Ala | Leu | Ser | Asn |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| ACT | GGA | GAG | ATC | CCC | TTC | TAT | GGC | AAA | GCC | ATC | CCC | ATT | GAA | GCC | ATC | 1200 |

|                   |            |                   |                   |                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| Thr<br>385        | Gly        | Glu               | Ile               | Pro               | Phe<br>390 | Tyr               | Gly               | Lys               | Ala               | Ile<br>395        | Pro               | Ile               | Glu               | Ala               | Ile<br>400        |      |
| AGG<br>Arg        | GGG<br>Gly | GGA<br>Gly        | AGG<br>Arg        | CAT<br>His<br>405 | CTC<br>Leu | ATT<br>Ile        | TTC<br>Phe        | TGT<br>Cys        | CAT<br>His<br>410 | TCC<br>Ser        | AAG<br>Lys        | AAG<br>Lys        | AAG<br>Lys        | TGC<br>Cys<br>415 | GAC<br>Asp        | 1248 |
| GAG<br>Glu        | CTC<br>Leu | GCC<br>Ala        | GCA<br>Ala<br>420 | AAG<br>Lys        | CTG<br>Leu | TCA<br>Ser        | GGC<br>Gly        | CTC<br>Leu<br>425 | GGA<br>Gly        | ATC<br>Ile        | AAC<br>Asn        | GCT<br>Ala        | GTG<br>Val<br>430 | GCG<br>Ala        | TAT<br>Tyr        | 1296 |
| TAC<br>Tyr        | CGG<br>Arg | GGG<br>Gly<br>435 | CTC<br>Leu        | GAT<br>Asp        | GTG<br>Val | TCC<br>Ser        | GTC<br>Val<br>440 | ATA<br>Ile        | CCA<br>Pro        | ACT<br>Thr        | ATC<br>Ile        | GGA<br>Gly<br>445 | GAC<br>Asp        | GTC<br>Val        | GTT<br>Val        | 1344 |
| GTC<br>Val<br>450 | GTG<br>Val | GCA<br>Ala        | ACA<br>Thr        | GAC<br>Asp        | GCT<br>Ala | CTG<br>Leu<br>455 | ATG<br>Met        | ACG<br>Thr        | GGC<br>Gly        | TAT<br>Tyr        | ACG<br>Thr<br>460 | GGC<br>Gly        | GAC<br>Asp        | TTT<br>Phe        | GAC<br>Asp        | 1392 |
| TCA<br>Ser<br>465 | GTG<br>Val | ATC<br>Ile        | GAC<br>Asp        | TGT<br>Cys<br>470 | AAC<br>Asn | ACA<br>Thr        | TGT<br>Cys        | GTC<br>Val        | ACC<br>Thr        | CAG<br>Gln<br>475 | ACA<br>Thr        | GTC<br>Val        | GAC<br>Asp        | TTC<br>Phe        | AGC<br>Ser<br>480 | 1440 |
| TTG<br>Leu        | GAT<br>Asp | CCC<br>Pro        | ACC<br>Thr        | TTC<br>Phe<br>485 | ACC<br>Thr | ATT<br>Ile        | GAG<br>Glu        | ACG<br>Thr        | ACG<br>Thr<br>490 | ACC<br>Thr        | GTG<br>Val        | CCT<br>Pro        | CAA<br>Gln        | GAC<br>Asp<br>495 | GCA<br>Ala        | 1488 |
| GTG<br>Val        | TCG<br>Ser | CGC<br>Arg        | TCG<br>Ser<br>500 | CAG<br>Gln        | CGG<br>Arg | CGG<br>Arg        | GGT<br>Gly        | AGG<br>Arg<br>505 | ACT<br>Thr        | GGC<br>Gly        | AGG<br>Arg        | GGT<br>Gly        | AGG<br>Arg<br>510 | AGA<br>Arg        | GGC<br>Gly        | 1536 |
| ATC<br>Ile        | TAC<br>Tyr | AGG<br>Arg<br>515 | TTT<br>Phe        | GTG<br>Val        | ACT<br>Thr | CCG<br>Pro        | GGA<br>Gly<br>520 | GAA<br>Glu        | CGG<br>Arg        | CCC<br>Pro        | TCG<br>Ser        | GGC<br>Gly<br>525 | ATG<br>Met        | TTC<br>Phe        | GAT<br>Asp        | 1584 |
| TCC<br>Ser<br>530 | TCG<br>Ser | GTC<br>Val        | CTG<br>Leu        | TGT<br>Cys        | GAG<br>Glu | TGC<br>Cys<br>535 | TAT<br>Tyr        | GAC<br>Asp        | GCG<br>Ala        | GGC<br>Gly        | TGT<br>Cys<br>540 | GCT<br>Ala        | TGG<br>Trp        | TAC<br>Tyr        | GAG<br>Glu        | 1632 |
| CTC<br>Leu<br>545 | ACC<br>Thr | CCC<br>Pro        | GCC<br>Ala        | GAG<br>Glu<br>550 | ACC<br>Thr | TCG<br>Ser        | GTT<br>Val        | AGG<br>Arg        | TTG<br>Leu        | CGG<br>Arg<br>555 | GCC<br>Ala        | TAC<br>Tyr        | CTG<br>Leu        | AAC<br>Asn        | ACA<br>Thr<br>560 | 1680 |
| CCA<br>Pro        | GGG<br>Gly | TTG<br>Leu        | CCC<br>Pro        | GTT<br>Val<br>565 | TGC<br>Cys | CAG<br>Gln        | GAC<br>Asp        | CAC<br>His        | CTG<br>Leu<br>570 | GAG<br>Glu        | TTC<br>Phe        | TGG<br>Trp        | GAG<br>Glu        | AGT<br>Ser<br>575 | GTC<br>Val        | 1728 |
| TTC<br>Phe        | ACA<br>Thr | GGC<br>Gly<br>580 | CTC<br>Leu        | ACC<br>Thr        | CAT<br>His | ATA<br>Ile        | GAT<br>Asp        | GCA<br>Ala<br>585 | CAC<br>His        | TTC<br>Phe        | TTG<br>Leu        | TCC<br>Ser        | CAG<br>Gln<br>590 | ACC<br>Thr        | AAG<br>Lys        | 1776 |
| CAG<br>Gln        | GCA<br>Ala | GGA<br>Gly<br>595 | GAC<br>Asp        | AAC<br>Asn        | TTC<br>Phe | CCC<br>Pro        | TAC<br>Tyr<br>600 | CTG<br>Leu        | GTA<br>Val        | GCA<br>Ala        | TAC<br>Tyr        | CAA<br>Gln<br>605 | GCC<br>Ala        | ACG<br>Thr        | GTG<br>Val        | 1824 |
| TGC<br>Cys<br>610 | GCC<br>Ala | AGG<br>Arg        | GCT<br>Ala        | CAG<br>Gln        | GCC<br>Ala | CCA<br>Pro<br>615 | CCT<br>Pro        | CCA<br>Pro        | TCA<br>Ser        | TGG<br>Trp        | GAT<br>Asp<br>620 | CAA<br>Gln        | ATG<br>Met        | TGG<br>Trp        | AAG<br>Lys        | 1872 |



(2) INFORMATION FOR SEQ ID NO:112:

(A) LENGTH: 648 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..648

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GGC | AGC | AGC | CAT | CAT | CAT | CAT | CAT | CAC | AGC | AGC | GGC | CTG | GTG | CCG | 48  |
| Met | Gly | Ser | Ser | His | His | His | His | His | His | Ser | Ser | Gly | Leu | Val | Pro |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CGC | GGC | AGC | CAT | ATG | GGT | TCT | GTT | GTT | ATT | GTT | GGT | AGA | ATT | ATT | TTA | 96  |
| Arg | Gly | Ser | His | Met | Gly | Ser | Val | Val | Ile | Val | Gly | Arg | Ile | Ile | Leu |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| TCT | CCT | GCT | GGT | ATC | ACG | GCC | TAC | TCC | CAA | CAG | ACG | CGG | GGC | CTA | CTT | 144 |
| Ser | Pro | Ala | Gly | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu | Leu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| GGT | TGC | ATC | ATC | ACT | AGC | CTT | ACA | GGC | CGG | GAC | AAG | AAC | CAG | GTC | GAG | 192 |
| Gly | Cys | Ile | Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | Glu |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| GGA | GAG | GTT | CAG | GTG | GTT | TCC | ACC | GCA | ACA | CAA | TCC | TTC | CTG | GCG | ACC | 240 |
| Gly | Glu | Val | Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala | Thr |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| TGC | GTC | AAC | GGC | GTG | TGT | TGG | ACC | GTT | TAC | CAT | GGT | GCT | GGC | TCA | AAG | 288 |
| Cys | Val | Asn | Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser | Lys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG | 336 |
| Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val |     |
| 100 105 110                                                     |     |
| GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG | 384 |
| Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu |     |
| 115 120 125                                                     |     |
| ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT | 432 |
| Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His |     |
| 130 135 140                                                     |     |
| GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG | 480 |
| Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu |     |
| 145 150 155 160                                                 |     |
| CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA | 528 |
| Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro |     |
| 165 170 175                                                     |     |
| CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA | 576 |
| Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val |     |
| 180 185 190                                                     |     |
| TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC | 624 |
| Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser |     |
| 195 200 205                                                     |     |
| ATG GAA ACT ACT ATG CGG TCT TGA                                 | 648 |
| Met Glu Thr Thr Met Arg Ser *                                   |     |
| 210 215                                                         |     |

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..640

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

|                                                                 |    |
|-----------------------------------------------------------------|----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48 |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |    |
| 1 5 10 15                                                       |    |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96 |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT | 144 |
| Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu |     |
| 35 40 45                                                        |     |
| GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG | 192 |
| Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu |     |
| 50 55 60                                                        |     |
| GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC | 240 |
| Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr |     |
| 65 70 75 80                                                     |     |
| TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG | 288 |
| Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys |     |
| 85 90 95                                                        |     |
| ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG | 336 |
| Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val |     |
| 100 105 110                                                     |     |
| GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG | 384 |
| Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu |     |
| 115 120 125                                                     |     |
| ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT | 432 |
| Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His |     |
| 130 135 140                                                     |     |
| GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG | 480 |
| Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu |     |
| 145 150 155 160                                                 |     |
| CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA | 528 |
| Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro |     |
| 165 170 175                                                     |     |
| CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA | 576 |
| Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val |     |
| 180 185 190                                                     |     |
| TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC | 624 |
| Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser |     |
| 195 200 205                                                     |     |
| ATG GAA ACT ACT ATG C GGTCTTGA                                  | 648 |
| Met Glu Thr Thr Met                                             |     |
| 210                                                             |     |

## (2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG | 48  |
| Met Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu |     |
| 1 5 10 15                                                       |     |
| GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC | 96  |
| Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val |     |
| 20 25 30                                                        |     |
| AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA | 144 |
| Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu |     |
| 35 40 45                                                        |     |
| GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG | 192 |
| Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln |     |
| 50 55 60                                                        |     |
| GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA | 240 |
| Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro |     |
| 65 70 75 80                                                     |     |
| TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC | 288 |
| Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp |     |
| 85 90 95                                                        |     |
| GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC | 336 |
| Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser |     |
| 100 105 110                                                     |     |
| CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC | 384 |
| Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu |     |
| 115 120 125                                                     |     |
| TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC | 432 |
| Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr |     |
| 130 135 140                                                     |     |
| CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA | 480 |
| Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu |     |
| 145 150 155 160                                                 |     |
| ACT ACT ATG CGG TCT TGA                                         | 498 |
| Thr Thr Met Arg Ser *                                           |     |
| 165                                                             |     |

20250101 11:00:00

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG | 48  |
| Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro |     |
| 1 5 10 15                                                       |     |
| CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA | 96  |
| Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu |     |
| 20 25 30                                                        |     |
| TCT GGT GGT TCT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT | 144 |
| Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu |     |
| 35 40 45                                                        |     |
| GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG | 192 |
| Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu |     |
| 50 55 60                                                        |     |
| GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC | 240 |
| Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr |     |
| 65 70 75 80                                                     |     |
| TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG | 288 |
| Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys |     |
| 85 90 95                                                        |     |
| ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG | 336 |
| Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val |     |
| 100 105 110                                                     |     |
| GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG | 384 |
| Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu |     |
| 115 120 125                                                     |     |
| ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT | 432 |
| Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His |     |
| 130 135 140                                                     |     |
| GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG | 480 |
| Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu |     |
| 145 150 155 160                                                 |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA | 528 |
| Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro |     |
| 165 170 175                                                     |     |
|                                                                 |     |
| CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA | 576 |
| Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val |     |
| 180 185 190                                                     |     |
|                                                                 |     |
| TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC | 624 |
| Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser |     |
| 195 200 205                                                     |     |
|                                                                 |     |
| ATG GAA ACT ACT ATG CGG TCT TGA                                 | 648 |
| Met Glu Thr Thr Met Arg Ser *                                   |     |
| 210 215                                                         |     |

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2004

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG | 48  |
| Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala |     |
| 1 5 10 15                                                       |     |
|                                                                 |     |
| CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC AAG | 96  |
| Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys |     |
| 20 25 30                                                        |     |
|                                                                 |     |
| ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT | 144 |
| Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val |     |
| 35 40 45                                                        |     |
|                                                                 |     |
| CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC | 192 |
| Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn |     |
| 50 55 60                                                        |     |
|                                                                 |     |
| GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC | 240 |
| Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala |     |
| 65 70 75 80                                                     |     |
|                                                                 |     |
| GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC | 288 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn | Val | Asp | Gln | Asp |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| CTC | GTC | GGC | TGG | CAG | GCG | CCC | CCC | GGG | GCG | CGT | TCC | TTG | ACA | CCA | TGC | 336 |
| Leu | Val | Gly | Trp | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser | Leu | Thr | Pro | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| ACC | TGT | GGC | AGC | TCA | GAC | CTT | TAC | TTG | GTC | ACG | AGA | CAT | GCT | GAC | GTC | 384 |
| Thr | Cys | Gly | Ser | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg | His | Ala | Asp | Val |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| ATT | CCG | GTG | CGC | CGG | CGG | GGC | GAC | AGT | AGG | GGG | AGC | CTG | CTC | TCC | CCC | 432 |
| Ile | Pro | Val | Arg | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser | Leu | Leu | Ser | Pro |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| AGG | CCT | GTC | TCC | TAC | TTG | AAG | GGC | TCT | TCG | GGT | GGT | CCA | CTG | CTC | TGC | 480 |
| Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ser | Gly | Gly | Pro | Leu | Leu | Cys |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| CCT | TCG | GGG | CAC | GCT | GTG | GGC | ATC | TTC | CGG | GCT | GCC | GTA | TGC | ACC | CGG | 528 |
| Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala | Val | Cys | Thr | Arg |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| GGG | GTT | GCG | AAG | GCG | GTG | GAC | TTT | GTG | CCC | GTA | GAG | TCC | ATG | GAA | ACT | 576 |
| Gly | Val | Ala | Lys | Ala | Val | Asp | Phe | Val | Pro | Val | Glu | Ser | Met | Glu | Thr |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| ACT | ATG | CGG | TCT | CCG | GTC | TTC | ACG | GAC | AAC | TCA | TCC | CCC | CCG | GCC | GTA | 624 |
| Thr | Met | Arg | Ser | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser | Pro | Pro | Ala | Val |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| CCG | CAG | TCA | TTT | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC | ACT | GGC | AGC | GGC | 672 |
| Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| AAG | AGT | ACT | AAA | GTG | CCG | GCT | GCA | TAT | GCA | GCC | CAA | GGG | TAC | AAG | GTG | 720 |
| Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | TTT | GGG | GCG | TAT | 768 |
| Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr |     |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | 816 |
| Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | 864 |
| Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | 912 |
| Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys |     |
|     | 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | GGC | ATC | GGC | ACA | 960 |
| Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GTC<br>Val        | CTG<br>Leu        | GAC<br>Asp        | CAA<br>Gln        | GCG<br>Ala<br>325 | GAG<br>Glu        | ACG<br>Thr        | GCT<br>Ala        | GGA<br>Gly        | GCG<br>Ala<br>330 | CGG<br>Arg        | CTT<br>Leu        | GTC<br>Val        | GTG<br>Val        | CTC<br>Leu<br>335 | GCC<br>Ala        | 1008 |
| ACC<br>Thr        | GCT<br>Ala        | ACG<br>Thr        | CCT<br>Pro<br>340 | CCG<br>Pro        | GGA<br>Gly        | TCG<br>Ser        | GTC<br>Val        | ACC<br>Thr<br>345 | GTG<br>Val        | CCA<br>Pro        | CAC<br>His        | CCA<br>Pro        | AAC<br>Asn<br>350 | ATC<br>Ile        | GAG<br>Glu        | 1056 |
| GAG<br>Glu        | GTG<br>Val        | GCC<br>Ala<br>355 | CTG<br>Leu        | TCT<br>Ser        | AAT<br>Asn        | ACT<br>Thr        | GGA<br>Gly<br>360 | GAG<br>Glu        | ATC<br>Ile        | CCC<br>Pro        | TTC<br>Phe        | TAT<br>Tyr<br>365 | GGC<br>Gly        | AAA<br>Lys        | GCC<br>Ala        | 1104 |
| ATC<br>Ile        | CCC<br>Pro<br>370 | ATT<br>Ile        | GAA<br>Glu        | GCC<br>Ala        | ATC<br>Ile        | AGG<br>Arg<br>375 | GGG<br>Gly        | GGA<br>Gly        | AGG<br>Arg        | CAT<br>His        | CTC<br>Leu<br>380 | ATT<br>Ile        | TTC<br>Phe        | TGT<br>Cys        | CAT<br>His        | 1152 |
| TCC<br>Ser<br>385 | AAG<br>Lys        | AAG<br>Lys        | AAG<br>Lys        | TGC<br>Cys        | GAC<br>Asp<br>390 | GAG<br>Glu        | CTC<br>Leu        | GCC<br>Ala        | GCA<br>Ala        | AAG<br>Lys<br>395 | CTG<br>Leu        | TCA<br>Ser        | GGC<br>Gly        | CTC<br>Leu        | GGA<br>Gly<br>400 | 1200 |
| ATC<br>Ile        | AAC<br>Asn        | GCT<br>Ala        | GTG<br>Val        | GCG<br>Ala<br>405 | TAT<br>Tyr        | TAC<br>Tyr        | CGG<br>Arg        | GGG<br>Gly        | CTC<br>Leu<br>410 | GAT<br>Asp        | GTG<br>Val        | TCC<br>Ser        | GTC<br>Val        | ATA<br>Ile<br>415 | CCA<br>Pro        | 1248 |
| ACT<br>Thr        | ATC<br>Ile        | GGA<br>Gly        | GAC<br>Asp<br>420 | GTC<br>Val        | GTT<br>Val        | GTC<br>Val        | GTG<br>Val        | GCA<br>Ala<br>425 | ACA<br>Thr        | GAC<br>Asp        | GCT<br>Ala        | CTG<br>Leu        | ATG<br>Met<br>430 | ACG<br>Thr        | GGC<br>Gly        | 1296 |
| TAT<br>Tyr        | ACG<br>Thr        | GGC<br>Gly<br>435 | GAC<br>Asp        | TTT<br>Phe        | GAC<br>Asp        | TCA<br>Ser        | GTG<br>Val<br>440 | ATC<br>Ile        | GAC<br>Asp        | TGT<br>Cys        | AAC<br>Asn        | ACA<br>Thr<br>445 | TGT<br>Cys        | GTC<br>Val        | ACC<br>Thr        | 1344 |
| CAG<br>Gln        | ACA<br>Thr<br>450 | GTC<br>Val        | GAC<br>Asp        | TTC<br>Phe        | AGC<br>Ser        | TTG<br>Leu        | GAT<br>Asp<br>455 | CCC<br>Pro        | ACC<br>Thr        | TTC<br>Phe        | ACC<br>Thr<br>460 | ATT<br>Ile        | GAG<br>Glu        | ACG<br>Thr        | ACG<br>Thr        | 1392 |
| ACC<br>Thr<br>465 | GTG<br>Val        | CCT<br>Pro        | CAA<br>Gln        | GAC<br>Asp<br>470 | GCA<br>Ala        | GTG<br>Val        | TCG<br>Ser        | CGC<br>Arg        | TCG<br>Ser        | CAG<br>Gln<br>475 | CGG<br>Arg        | CGG<br>Arg        | GGT<br>Gly        | AGG<br>Arg        | ACT<br>Thr<br>480 | 1440 |
| GGC<br>Gly        | AGG<br>Arg        | GGT<br>Gly        | AGG<br>Arg<br>485 | AGA<br>Arg        | GGC<br>Gly        | ATC<br>Ile        | TAC<br>Tyr        | AGG<br>Arg<br>490 | TTT<br>Phe        | GTG<br>Val        | ACT<br>Thr        | CCG<br>Pro        | GGA<br>Gly        | GAA<br>Glu<br>495 | CGG<br>Arg        | 1488 |
| CCC<br>Pro        | TCG<br>Ser        | GGC<br>Gly        | ATG<br>Met<br>500 | TTC<br>Phe        | GAT<br>Asp        | TCC<br>Ser        | TCG<br>Ser        | GTC<br>Val<br>505 | CTG<br>Leu        | TGT<br>Cys        | GAG<br>Glu        | TGC<br>Cys        | TAT<br>Tyr<br>510 | GAC<br>Asp        | GCG<br>Ala        | 1536 |
| GGC<br>Gly        | TGT<br>Cys        | GCT<br>Ala<br>515 | TGG<br>Trp        | TAC<br>Tyr        | GAG<br>Glu        | CTC<br>Leu        | ACC<br>Thr<br>520 | CCC<br>Pro        | GCC<br>Ala        | GAG<br>Glu        | ACC<br>Thr        | TCG<br>Ser<br>525 | GTT<br>Val        | AGG<br>Arg        | TTG<br>Leu        | 1584 |
| CGG<br>Arg        | GCC<br>Ala<br>530 | TAC<br>Tyr        | CTG<br>Leu        | AAC<br>Asn        | ACA<br>Thr        | CCA<br>Pro<br>535 | GGG<br>Gly        | TTG<br>Leu        | CCC<br>Pro        | GTT<br>Val        | TGC<br>Cys<br>540 | CAG<br>Gln        | GAC<br>Asp        | CAC<br>His        | CTG<br>Leu        | 1632 |
| GAG               | TTC               | TGG               | GAG               | AGT               | GTC               | TTC               | ACA               | GGC               | CTC               | ACC               | CAT               | ATA               | GAT               | GCA               | CAC               | 1680 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His | Ile | Asp | Ala | His |      |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |      |  |
| TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | CCC | TAC | CTG | GTA | 1728 |  |
| Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe | Pro | Tyr | Leu | Val |      |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |      |  |
| GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | CCA | CCT | CCA | TCA | 1776 |  |
| Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala | Pro | Pro | Pro | Ser |      |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |  |
| TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | CCT | ACG | CTG | CAC | 1824 |  |
| Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys | Pro | Thr | Leu | His |      |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |      |  |
| GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | CAA | AAT | GAG | GTC | 1872 |  |
| Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val | Gln | Asn | Glu | Val |      |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |  |
| ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA | TGC | ATG | TCG | GCC | 1920 |  |
| Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala | Cys | Met | Ser | Ala |      |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |  |
| GAC | CTG | GAG | GTC | GTT | ACG | TAG | GAA | TTC | GAG | CTC | CGT | CGA | CAA | GCT | TGC | 1968 |  |
| Asp | Leu | Glu | Val | Val | Thr | *   | Glu | Phe | Glu | Leu | Arg | Arg | Gln | Ala | Cys |      |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |      |  |
| GGC | CGC | ACT | CGA | GCA | CCA | CCA | CCA | CCA | CCA | CTG | AGA | TCC |     |     |     | 2007 |  |
| Gly | Arg | Thr | Arg | Ala | Pro | Pro | Pro | Pro | Pro | Leu | Arg |     |     |     |     |      |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2004

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|--|
| ATG | CAT | ATG | CAT | CAT | CAT | CAC | CAT | CAT | CTG | GTG | CCG | CGC | GGC | AGC | GCG | 48 |  |
| Met | His | Met | His | His | His | His | His | His | Leu | Val | Pro | Arg | Gly | Ser | Ala |    |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |    |  |
| CCC | ATC | ACG | GCC | TAC | TCC | CAA | CAG | ACG | CGG | GGC | CTA | CTT | GGT | TGC | ATC | 96 |  |
| Pro | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu | Leu | Gly | Cys | Ile |    |  |

| 20         |            |            |            | 25         |            |            |            | 30         |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| AAG<br>Lys | ACT<br>Thr | AGC<br>Ser | CTT<br>Leu | ACA<br>Thr | GGC<br>Gly | CGG<br>Arg | GAC<br>Asp | AAG<br>Lys | AAC<br>Asn | CAG<br>Gln | GTC<br>Val | GAG<br>Glu | GGA<br>Gly | GAG<br>Glu | GTT<br>Val | 144 |
| 35         |            |            | 40         |            |            |            | 45         |            |            |            |            |            |            |            |            |     |
| CAG<br>Gln | GTG<br>Val | GTT<br>Val | TCC<br>Ser | ACC<br>Thr | GCA<br>Ala | ACA<br>Thr | CAA<br>Gln | TCC<br>Ser | TTC<br>Phe | CTG<br>Leu | GCG<br>Ala | ACC<br>Thr | TGC<br>Cys | GTC<br>Val | AAC<br>Asn | 192 |
| 50         |            |            | 55         |            |            |            | 60         |            |            |            |            |            |            |            |            |     |
| GGC<br>Gly | GTG<br>Val | TGT<br>Cys | TGG<br>Trp | ACC<br>Thr | GTT<br>Val | TAC<br>Tyr | CAT<br>His | GGT<br>Gly | GCT<br>Ala | GGC<br>Gly | TCA<br>Ser | AAG<br>Lys | ACC<br>Thr | TTA<br>Leu | GCC<br>Ala | 240 |
| 65         |            |            | 70         |            |            |            | 75         |            |            |            | 80         |            |            |            |            |     |
| GGC<br>Gly | CCA<br>Pro | AAG<br>Lys | GGG<br>Gly | CCA<br>Pro | ATC<br>Ile | ACC<br>Thr | CAG<br>Gln | ATG<br>Met | TAC<br>Tyr | ACT<br>Thr | AAT<br>Asn | GTG<br>Val | GAC<br>Asp | CAG<br>Gln | GAC<br>Asp | 288 |
| 85         |            |            | 90         |            |            |            | 95         |            |            |            |            |            |            |            |            |     |
| CTC<br>Leu | GTC<br>Val | GGC<br>Gly | TGG<br>Trp | CAG<br>Gln | GCG<br>Ala | CCC<br>Pro | CCC<br>Pro | GGG<br>Gly | GCG<br>Ala | CGT<br>Arg | TCC<br>Ser | TTG<br>Leu | ACA<br>Thr | CCA<br>Pro | TGC<br>Cys | 336 |
| 100        |            |            | 105        |            |            |            | 110        |            |            |            |            |            |            |            |            |     |
| ACC<br>Thr | TGT<br>Cys | GGC<br>Gly | AGC<br>Ser | TCA<br>Ser | GAC<br>Asp | CTT<br>Leu | TAC<br>Tyr | TTG<br>Leu | GTC<br>Val | ACG<br>Thr | AGA<br>Arg | CAT<br>His | GCT<br>Ala | GAC<br>Asp | GTC<br>Val | 384 |
| 115        |            |            | 120        |            |            |            | 125        |            |            |            |            |            |            |            |            |     |
| ATT<br>Ile | CCG<br>Pro | GTG<br>Val | CGC<br>Arg | CGG<br>Arg | CGG<br>Arg | GGC<br>Gly | GAC<br>Asp | AGT<br>Ser | AGG<br>Arg | GGG<br>Gly | AGC<br>Ser | CTG<br>Leu | CTC<br>Leu | TCC<br>Ser | CCC<br>Pro | 432 |
| 130        |            |            | 135        |            |            |            | 140        |            |            |            |            |            |            |            |            |     |
| AGG<br>Arg | CCT<br>Pro | GTC<br>Val | TCC<br>Ser | TAC<br>Tyr | TTG<br>Leu | AAG<br>Lys | GGC<br>Gly | TCT<br>Ser | TCG<br>Ser | GGT<br>Gly | GGT<br>Gly | CCA<br>Pro | CTG<br>Leu | CTC<br>Leu | TGC<br>Cys | 480 |
| 145        |            |            | 150        |            |            |            | 155        |            |            |            | 160        |            |            |            |            |     |
| CCT<br>Pro | TCG<br>Ser | GGG<br>Gly | CAC<br>His | GCT<br>Ala | GTG<br>Val | GGC<br>Gly | ATC<br>Ile | TTC<br>Phe | CGG<br>Arg | GCT<br>Ala | GCC<br>Ala | GTA<br>Val | TGC<br>Cys | ACC<br>Thr | CGG<br>Arg | 528 |
| 165        |            |            | 170        |            |            |            | 175        |            |            |            |            |            |            |            |            |     |
| GGG<br>Gly | GTT<br>Val | GCG<br>Ala | AAG<br>Lys | GCG<br>Ala | GTG<br>Val | GAC<br>Asp | TTT<br>Phe | GTG<br>Val | CCC<br>Pro | GTA<br>Val | GAG<br>Glu | TCC<br>Ser | ATG<br>Met | GAA<br>Glu | ACT<br>Thr | 576 |
| 180        |            |            | 185        |            |            |            | 190        |            |            |            |            |            |            |            |            |     |
| ACT<br>Thr | ATG<br>Met | CGG<br>Arg | TCT<br>Ser | CCG<br>Pro | GTC<br>Val | TTC<br>Phe | ACG<br>Thr | GAC<br>Asp | AAC<br>Asn | TCA<br>Ser | TCC<br>Ser | CCC<br>Pro | CCG<br>Pro | GCC<br>Ala | GTA<br>Val | 624 |
| 195        |            |            | 200        |            |            |            | 205        |            |            |            |            |            |            |            |            |     |
| CCG<br>Pro | CAG<br>Gln | TCA<br>Ser | TTT<br>Phe | CAA<br>Gln | GTG<br>Val | GCC<br>Ala | CAC<br>His | CTA<br>Leu | CAC<br>His | GCT<br>Ala | CCC<br>Pro | ACT<br>Thr | GGC<br>Gly | AGC<br>Ser | GGC<br>Gly | 672 |
| 210        |            |            | 215        |            |            |            | 220        |            |            |            |            |            |            |            |            |     |
| AAG<br>Lys | AGT<br>Ser | ACT<br>Thr | AAA<br>Lys | GTG<br>Val | CCG<br>Pro | GCT<br>Ala | GCA<br>Ala | TAT<br>Tyr | GCA<br>Ala | GCC<br>Ala | CAA<br>Gln | GGG<br>Gly | TAC<br>Tyr | AAG<br>Lys | GTG<br>Val | 720 |
| 225        |            |            | 230        |            |            |            | 235        |            |            |            | 240        |            |            |            |            |     |
| CTC<br>Leu | GTC<br>Val | CTC<br>Leu | AAT<br>Asn | CCG<br>Pro | TCC<br>Ser | GTT<br>Val | GCC<br>Ala | GCT<br>Ala | ACC<br>Thr | TTA<br>Leu | GGG<br>Gly | TTT<br>Phe | GGG<br>Gly | GCG<br>Ala | TAT<br>Tyr | 768 |
| 245        |            |            | 250        |            |            |            | 255        |            |            |            |            |            |            |            |            |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | 816  |
| Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | 864  |
| Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | 912  |
| Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | GGC | ATC | GGC | ACA | 960  |
| Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT | GTC | GTG | CTC | GCC | 1008 |
| Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala |      |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |      |
| ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | CCA | AAC | ATC | GAG | 1056 |
| Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | TAT | GGC | AAA | GCC | 1104 |
| Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | ATT | TTC | TGT | CAT | 1152 |
| Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | TCA | GGC | CTC | GGA | 1200 |
| Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | TCC | GTC | ATA | CCA | 1248 |
| Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | CTG | ATG | ACG | GGC | 1296 |
| Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala | Leu | Met | Thr | Gly |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | ACA | TGT | GTC | ACC | 1344 |
| Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn | Thr | Cys | Val | Thr |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | ATT | GAG | ACG | ACG | 1392 |
| Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr | Ile | Glu | Thr | Thr |      |
|     |     | 450 |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |      |
| ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | CGG | GGT | AGG | ACT | 1440 |
| Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg | Arg | Gly | Arg | Thr |      |
|     |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |
| GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | CCG | GGA | GAA | CGG | 1488 |
| Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr | Pro | Gly | Glu | Arg |      |

| 485                                                                                                                                                   | 490 | 495 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG<br>Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala<br>500 505 510     |     |     | 1536 |
| GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG<br>Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu<br>515 520 525     |     |     | 1584 |
| CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG<br>Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu<br>530 535 540     |     |     | 1632 |
| GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC<br>Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His<br>545 550 555 560 |     |     | 1680 |
| TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA<br>Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val<br>565 570 575     |     |     | 1728 |
| GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA<br>Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser<br>580 585 590     |     |     | 1776 |
| TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC<br>Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His<br>595 600 605     |     |     | 1824 |
| GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC<br>Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val<br>610 615 620     |     |     | 1872 |
| ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC<br>Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala<br>625 630 635 640 |     |     | 1920 |
| GAC CTG GAG GTC GTT ACG TAG GAA TTC GAG CTC CGT CGA CAA GCT TGC<br>Asp Leu Glu Val Val Thr * Glu Phe Glu Leu Arg Arg Gln Ala Cys<br>645 650 655       |     |     | 1968 |
| GGC CGC ACT CGA GCA CCA CCA CCA CCA CCA CTG AGA TCC<br>Gly Arg Thr Arg Ala Pro Pro Pro Pro Pro Leu Arg<br>660 665                                     |     |     | 2007 |

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2004

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG | 48  |
| Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala |     |
| 1 5 10 15                                                       |     |
| CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC | 96  |
| Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile |     |
| 20 25 30                                                        |     |
| ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT | 144 |
| Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val |     |
| 35 40 45                                                        |     |
| CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC | 192 |
| Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn |     |
| 50 55 60                                                        |     |
| GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC | 240 |
| Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala |     |
| 65 70 75 80                                                     |     |
| GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC | 288 |
| Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp |     |
| 85 90 95                                                        |     |
| CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC | 336 |
| Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys |     |
| 100 105 110                                                     |     |
| ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC | 384 |
| Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val |     |
| 115 120 125                                                     |     |
| ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC | 432 |
| Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro |     |
| 130 135 140                                                     |     |
| AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT CCA CTG CTC TGC | 480 |
| Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys |     |
| 145 150 155 160                                                 |     |
| CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG | 528 |
| Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg |     |
| 165 170 175                                                     |     |
| GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC ATG GAA ACT | 576 |
| Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr |     |
| 180 185 190                                                     |     |
| ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC CCC CCG GCC GTA | 624 |
| Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val |     |
| 195 200 205                                                     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CCG | CAG | TCA | TTT | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC | ACT | GGC | AGC | GGC | 672  |
| Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly |      |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| AAG | AGT | ACT | AAA | GTG | CCG | GCT | GCA | TAT | GCA | GCC | CAA | GGG | TAC | AAG | GTG | 720  |
| Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | TTT | GGG | GCG | TAT | 768  |
| Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | 816  |
| Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | 864  |
| Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | 912  |
| Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | GGC | ATC | GGC | ACA | 960  |
| Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT | GTC | GTG | CTC | GCC | 1008 |
| Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | CCA | AAC | ATC | GAG | 1056 |
| Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | TAT | GGC | AAA | GCC | 1104 |
| Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | ATT | TTC | TGT | CAT | 1152 |
| Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | TCA | GGC | CTC | GGA | 1200 |
| Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | TCC | GTC | ATA | CCA | 1248 |
| Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | CTG | ATG | ACG | GGC | 1296 |
| Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala | Leu | Met | Thr | Gly |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | ACA | TGT | GTC | ACC | 1344 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn | Thr | Cys | Val | Thr |      |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |  |
| CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | ATT | GAG | ACG | ACG | 1392 |  |
| Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr | Ile | Glu | Thr | Thr |      |  |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |  |
| ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | CGG | GGT | AGG | ACT | 1440 |  |
| Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg | Arg | Gly | Arg | Thr |      |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |      |  |
| GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | CCG | GGA | GAA | CGG | 1488 |  |
| Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr | Pro | Gly | Glu | Arg |      |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |  |
| CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | TGC | TAT | GAC | GCG | 1536 |  |
| Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu | Cys | Tyr | Asp | Ala |      |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     |     | 510 |     |      |  |
| GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | TCG | GTT | AGG | TTG | 1584 |  |
| Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr | Ser | Val | Arg | Leu |      |  |
|     |     | 515 |     |     |     | 520 |     |     |     |     |     | 525 |     |     |     |      |  |
| CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | CAG | GAC | CAC | CTG | 1632 |  |
| Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys | Gln | Asp | His | Leu |      |  |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |      |  |
| GAG | TTC | TGG | GAG | AGT | GTC | TTC | ACA | GGC | CTC | ACC | CAT | ATA | GAT | GCA | CAC | 1680 |  |
| Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His | Ile | Asp | Ala | His |      |  |
| 545 |     |     |     |     | 550 |     |     |     | 555 |     |     |     |     |     | 560 |      |  |
| TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | CCC | TAC | CTG | GTA | 1728 |  |
| Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe | Pro | Tyr | Leu | Val |      |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |      |  |
| GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | CCA | CCT | CCA | TCA | 1776 |  |
| Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala | Pro | Pro | Pro | Ser |      |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |  |
| TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | CCT | ACG | CTG | CAC | 1824 |  |
| Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys | Pro | Thr | Leu | His |      |  |
|     |     | 595 |     |     |     | 600 |     |     |     |     |     | 605 |     |     |     |      |  |
| GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | CAA | AAT | GAG | GTC | 1872 |  |
| Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val | Gln | Asn | Glu | Val |      |  |
|     |     | 610 |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |  |
| ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA | TGC | ATG | TCG | GCC | 1920 |  |
| Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala | Cys | Met | Ser | Ala |      |  |
| 625 |     |     |     |     | 630 |     |     |     | 635 |     |     |     |     |     | 640 |      |  |
| GAC | CTG | GAG | GTC | GTT | ACG | TAG | GAA | TTC | GAG | CTC | CGT | CGA | CAA | GCT | TGC | 1968 |  |
| Asp | Leu | Glu | Val | Val | Thr | *   | Glu | Phe | Glu | Leu | Arg | Arg | Gln | Ala | Cys |      |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |      |  |
| GGC | CGC | ACT | CGA | GCA | CCA | CCA | CCA | CCA | CCA | CTG | AGA | TCC |     |     |     | 2007 |  |
| Gly | Arg | Thr | Arg | Ala | Pro | Pro | Pro | Pro | Pro | Leu | Arg |     |     |     |     |      |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     |     |     |     |      |  |

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2004

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG | 48  |
| Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala |     |
| 1 5 10 15                                                       |     |
| CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC | 96  |
| Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile |     |
| 20 25 30                                                        |     |
| ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT | 144 |
| Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val |     |
| 35 40 45                                                        |     |
| CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC | 192 |
| Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn |     |
| 50 55 60                                                        |     |
| GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC | 240 |
| Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala |     |
| 65 70 75 80                                                     |     |
| GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC | 288 |
| Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp |     |
| 85 90 95                                                        |     |
| CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC | 336 |
| Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys |     |
| 100 105 110                                                     |     |
| ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC | 384 |
| Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val |     |
| 115 120 125                                                     |     |
| ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC | 432 |
| Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro |     |
| 130 135 140                                                     |     |
| AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC | 480 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Arg | Pro | Val | Ser | Tyr | Leu | Lys | Gly | Ser | Ser | Gly | Gly | Pro | Leu | Leu | Cys |      |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |      |
| CCT | TCG | GGG | CAC | GCT | GTG | GGC | ATC | TTC | CGG | GCT | GCC | GTA | TGC | ACC | CGG | 528  |
| Pro | Ser | Gly | His | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala | Val | Cys | Thr | Arg |      |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |      |
| GGG | GTT | GCG | AAG | GCG | GTG | GAC | TTT | GTG | CCC | GTA | GAG | TCC | ATG | GAA | ACT | 576  |
| Gly | Val | Ala | Lys | Ala | Val | Asp | Phe | Val | Pro | Val | Glu | Ser | Met | Glu | Thr |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| ACT | ATG | CGG | TCT | CCG | GTC | TTC | ACG | GAC | AAC | TCA | TCC | CCC | CCG | GCC | GTA | 624  |
| Thr | Met | Arg | Ser | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser | Pro | Pro | Ala | Val |      |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| CCG | CAG | TCA | TTT | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC | ACT | GGC | AGC | GGC | 672  |
| Pro | Gln | Ser | Phe | Gln | Val | Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly |      |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| AAG | AGT | ACT | AAA | GTG | CCG | GCT | GCA | TAT | GCA | GCC | CAA | GGG | TAC | AAG | GTG | 720  |
| Lys | Ser | Thr | Lys | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| CTC | GTC | CTC | AAT | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | TTT | GGG | GCG | TAT | 768  |
| Leu | Val | Leu | Asn | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| ATG | TCT | AAG | GCA | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | 816  |
| Met | Ser | Lys | Ala | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| ACC | ATT | ACC | ACA | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | 864  |
| Thr | Ile | Thr | Thr | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| CTT | GCC | GAT | GGT | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | 912  |
| Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys |      |
|     | 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |      |
| GAT | GAG | TGC | CAT | TCA | ACT | GAC | TCG | ACT | ACA | ATC | TTG | GGC | ATC | GGC | ACA | 960  |
| Asp | Glu | Cys | His | Ser | Thr | Asp | Ser | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| GTC | CTG | GAC | CAA | GCG | GAG | ACG | GCT | GGA | GCG | CGG | CTT | GTC | GTG | CTC | GCC | 1008 |
| Val | Leu | Asp | Gln | Ala | Glu | Thr | Ala | Gly | Ala | Arg | Leu | Val | Val | Leu | Ala |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | CCA | AAC | ATC | GAG | 1056 |
| Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | TAT | GGC | AAA | GCC | 1104 |
| Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | ATT | TTC | TGT | CAT | 1152 |
| Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | TCA | GGC | CTC | GGA | 1200 |
| Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | TCC | GTC | ATA | CCA | 1248 |
| Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| ACT | TCC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | CTG | ATG | ACG | GGC | 1296 |
| Thr | Ser | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala | Leu | Met | Thr | Gly |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | ACA | TGT | GTC | ACC | 1344 |
| Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn | Thr | Cys | Val | Thr |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |      |
| CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | ATT | GAG | ACG | ACG | 1392 |
| Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr | Ile | Glu | Thr | Thr |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |      |
| ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | CGG | GGT | AGG | ACT | 1440 |
| Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg | Arg | Gly | Arg | Thr |      |
| 465 |     |     |     |     | 470 |     |     |     | 475 |     |     |     |     |     | 480 |      |
| GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | CCG | GGA | GAA | CGG | 1488 |
| Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr | Pro | Gly | Glu | Arg |      |
|     |     |     |     | 485 |     |     |     | 490 |     |     |     |     |     | 495 |     |      |
| CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | TGC | TAT | GAC | GCG | 1536 |
| Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu | Cys | Tyr | Asp | Ala |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |
| GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | TCG | GTT | AGG | TTG | 1584 |
| Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr | Ser | Val | Arg | Leu |      |
|     |     | 515 |     |     |     | 520 |     |     |     |     |     | 525 |     |     |     |      |
| CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | CAG | GAC | CAC | CTG | 1632 |
| Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys | Gln | Asp | His | Leu |      |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |      |
| GAG | TTC | TGG | GAG | AGT | GTC | TTC | ACA | GGC | CTC | ACC | CAT | ATA | GAT | GCA | CAC | 1680 |
| Glu | Phe | Trp | Glu | Ser | Val | Phe | Thr | Gly | Leu | Thr | His | Ile | Asp | Ala | His |      |
| 545 |     |     |     |     | 550 |     |     |     | 555 |     |     |     |     | 560 |     |      |
| TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | CCC | TAC | CTG | GTA | 1728 |
| Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe | Pro | Tyr | Leu | Val |      |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |      |
| GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | CCA | CCT | CCA | TCA | 1776 |
| Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala | Pro | Pro | Pro | Ser |      |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |
| TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | CCT | ACG | CTG | CAC | 1824 |
| Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys | Pro | Thr | Leu | His |      |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |      |
| GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | CAA | AAT | GAG | GTC | 1872 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val | Gln | Asn | Glu | Val |      |
| 610 |     |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |
| ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA | TGC | ATG | TCG | GCC | 1920 |
| Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala | Cys | Met | Ser | Ala |      |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |
| GAC | CTG | GAG | GTC | GTT | ACG | TAG | GAA | TTC | GAG | CTC | CGT | CGA | CAA | GCT | TGC | 1968 |
| Asp | Leu | Glu | Val | Val | Thr | *   | Glu | Phe | Glu | Leu | Arg | Arg | Gln | Ala | Cys |      |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |      |
| GGC | CGC | ACT | CGA | GCA | CCA | CCA | CCA | CCA | CCA | CTG | AGA | TCC |     |     |     | 2007 |
| Gly | Arg | Thr | Arg | Ala | Pro | Pro | Pro | Pro | Pro | Leu | Arg |     |     |     |     |      |
|     |     |     |     | 660 |     |     |     |     | 665 |     |     |     |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2007

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | CAT | ATG | CAT | CAT | CAT | CAC | CAT | CAT | CTG | GTG | CCG | CGC | GGC | AGC | GCG | 48  |
| Met | His | Met | His | His | His | His | His | His | Leu | Val | Pro | Arg | Gly | Ser | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CCC | ATC | ACG | GCC | TAC | TCC | CAA | CAG | ACG | CGG | GGC | CTA | CTT | GGT | TGC | ATC | 96  |
| Pro | Ile | Thr | Ala | Tyr | Ser | Gln | Gln | Thr | Arg | Gly | Leu | Leu | Gly | Cys | Ile |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| ATC | ACT | AGC | CTT | ACA | GGC | CGG | GAC | AAG | AAC | CAG | GTC | GAG | GGA | GAG | GTT | 144 |
| Ile | Thr | Ser | Leu | Thr | Gly | Arg | Asp | Lys | Asn | Gln | Val | Glu | Gly | Glu | Val |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| CAG | GTG | GTT | TCC | ACC | GCA | ACA | CAA | TCC | TTC | CTG | GCG | ACC | TGC | GTC | AAC | 192 |
| Gln | Val | Val | Ser | Thr | Ala | Thr | Gln | Ser | Phe | Leu | Ala | Thr | Cys | Val | Asn |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| GGC | GTG | TGT | TGG | ACC | GTT | TAC | CAT | GGT | GCT | GGC | TCA | AAG | ACC | TTA | GCC | 240 |
| Gly | Val | Cys | Trp | Thr | Val | Tyr | His | Gly | Ala | Gly | Ser | Lys | Thr | Leu | Ala |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| GGC | CCA | AAG | GGG | CCA | ATC | ACC | CAG | ATG | TAC | ACT | AAT | GTG | GAC | CAG | GAC | 288 |
| Gly | Pro | Lys | Gly | Pro | Ile | Thr | Gln | Met | Tyr | Thr | Asn | Val | Asp | Gln | Asp |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|     |     |     |       |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTC | GTC | GGC | TGG   | CAG | GCG | CCC | CCC | GGG | GCG | CGT | TCC | TTG | ACA | CCA | TGC | 336 |
| Leu | Val | Gly | Trp   | Gln | Ala | Pro | Pro | Gly | Ala | Arg | Ser | Leu | Thr | Pro | Cys |     |
|     |     | 100 |       |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| ACC | TGT | GGC | AGC   | TCA | GAC | CTT | TAC | TTG | GTC | ACG | AGA | CAT | GCT | GAC | GTC | 384 |
| Thr | Cys | Gly | Ser   | Ser | Asp | Leu | Tyr | Leu | Val | Thr | Arg | His | Ala | Asp | Val |     |
|     |     | 115 |       |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| ATT | CCG | GTG | CGC   | CGG | CGG | GGC | GAC | AGT | AGG | GGG | AGC | CTG | CTC | TCC | CCC | 432 |
| Ile | Pro | Val | Arg   | Arg | Arg | Gly | Asp | Ser | Arg | Gly | Ser | Leu | Leu | Ser | Pro |     |
|     | 130 |     |       |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| AGG | CCT | GTC | TCC   | TAC | TTG | AAG | GGC | TCT | TCG | GGT | GGT | CCA | CTG | CTC | TGC | 480 |
| Arg | Pro | Val | Ser   | Tyr | Leu | Lys | Gly | Ser | Ser | Gly | Gly | Pro | Leu | Leu | Cys |     |
| 145 |     |     |       |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| CCT | TCG | GGG | CAC   | GCT | GTG | GGC | ATC | TTC | CGG | GCT | GCC | GTA | TGC | ACC | CGG | 528 |
| Pro | Ser | Gly | His   | Ala | Val | Gly | Ile | Phe | Arg | Ala | Ala | Val | Cys | Thr | Arg |     |
|     |     |     | 165   |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| GGG | GTT | GCG | AAG   | GCG | GTG | GAC | TTT | GTG | CCC | GTA | GAG | TCC | ATG | GAA | ACT | 576 |
| Gly | Val | Ala | Lys   | Ala | Val | Asp | Phe | Val | Pro | Val | Glu | Ser | Met | Glu | Thr |     |
|     |     | 180 |       |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| ACT | ATG | CGG | TCT   | CCG | GTC | TTC | ACG | GAC | AAC | TCA | TCC | CCC | CCG | GCC | GTA | 624 |
| Thr | Met | Arg | Ser   | Pro | Val | Phe | Thr | Asp | Asn | Ser | Ser | Pro | Pro | Ala | Val |     |
|     | 195 |     |       |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| CCG | CAG | TCA | TTT   | CAA | GTG | GCC | CAC | CTA | CAC | GCT | CCC | ACT | GGC | AGC | GGC | 672 |
| Pro | Gln | Ser | Phe   | Gln | Val | Ala | His | Leu | His | Ala | Pro | Thr | Gly | Ser | Gly |     |
|     | 210 |     |       |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| AAG | AGT | ACT | AAA   | GTG | CCG | GCT | GCC | TAC | GCA | GCC | CAA | GGG | TAC | AAG | GTG | 720 |
| Lys | Ser | Thr | Lys   | Val | Pro | Ala | Ala | Tyr | Ala | Ala | Gln | Gly | Tyr | Lys | Val |     |
| 225 |     |     |       |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| CTC | GTC | CTC | AAT   | CCG | TCC | GTT | GCC | GCT | ACC | TTA | GGG | TTT | GGG | GCG | TAT | 768 |
| Leu | Val | Leu | Asn   | Pro | Ser | Val | Ala | Ala | Thr | Leu | Gly | Phe | Gly | Ala | Tyr |     |
|     |     |     | 245   |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| ATG | TCT | AAG | GCA   | CAC | GGT | ATT | GAC | CCC | AAC | ATC | AGA | ACT | GGG | GTA | AGG | 816 |
| Met | Ser | Lys | Ala   | His | Gly | Ile | Asp | Pro | Asn | Ile | Arg | Thr | Gly | Val | Arg |     |
|     |     | 260 |       |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| ACC | ATT | ACC | ACA   | GGC | GCC | CCC | GTC | ACA | TAC | TCT | ACC | TAT | GGC | AAG | TTT | 864 |
| Thr | Ile | Thr | Thr   | Gly | Ala | Pro | Val | Thr | Tyr | Ser | Thr | Tyr | Gly | Lys | Phe |     |
|     |     | 275 |       |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| CTT | GCC | GAT | GGT   | GGT | TGC | TCT | GGG | GGC | GCT | TAT | GAC | ATC | ATA | ATA | TGT | 912 |
| Leu | Ala | Asp | Gly   | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | Ile | Ile | Ile | Cys |     |
|     | 290 |     |       |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| GAT | GAG | TGC | CAT</ |     |     |     |     |     |     |     |     |     |     |     |     |     |

| 325 |     |     |     |     |     |     |     | 330 |     |     |     | 335 |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ACC | GCT | ACG | CCT | CCG | GGA | TCG | GTC | ACC | GTG | CCA | CAC | CCA | AAC | ATC | GAG | 1056 |
| Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Val | Pro | His | Pro | Asn | Ile | Glu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| GAG | GTG | GCC | CTG | TCT | AAT | ACT | GGA | GAG | ATC | CCC | TTC | TAT | GGC | AAA | GCC | 1104 |
| Glu | Val | Ala | Leu | Ser | Asn | Thr | Gly | Glu | Ile | Pro | Phe | Tyr | Gly | Lys | Ala |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| ATC | CCC | ATT | GAA | GCC | ATC | AGG | GGG | GGA | AGG | CAT | CTC | ATT | TTC | TGT | CAT | 1152 |
| Ile | Pro | Ile | Glu | Ala | Ile | Arg | Gly | Gly | Arg | His | Leu | Ile | Phe | Cys | His |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| TCC | AAG | AAG | AAG | TGC | GAC | GAG | CTC | GCC | GCA | AAG | CTG | TCA | GGC | CTC | GGA | 1200 |
| Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Ala | Lys | Leu | Ser | Gly | Leu | Gly |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| ATC | AAC | GCT | GTG | GCG | TAT | TAC | CGG | GGG | CTC | GAT | GTG | TCC | GTC | ATA | CCA | 1248 |
| Ile | Asn | Ala | Val | Ala | Tyr | Tyr | Arg | Gly | Leu | Asp | Val | Ser | Val | Ile | Pro |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| ACT | ATC | GGA | GAC | GTC | GTT | GTC | GTG | GCA | ACA | GAC | GCT | CTG | ATG | ACG | GGC | 1296 |
| Thr | Ile | Gly | Asp | Val | Val | Val | Val | Ala | Thr | Asp | Ala | Leu | Met | Thr | Gly |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| TAT | ACG | GGC | GAC | TTT | GAC | TCA | GTG | ATC | GAC | TGT | AAC | ACA | TGT | GTC | ACC | 1344 |
| Tyr | Thr | Gly | Asp | Phe | Asp | Ser | Val | Ile | Asp | Cys | Asn | Thr | Cys | Val | Thr |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| CAG | ACA | GTC | GAC | TTC | AGC | TTG | GAT | CCC | ACC | TTC | ACC | ATT | GAG | ACG | ACG | 1392 |
| Gln | Thr | Val | Asp | Phe | Ser | Leu | Asp | Pro | Thr | Phe | Thr | Ile | Glu | Thr | Thr |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| ACC | GTG | CCT | CAA | GAC | GCA | GTG | TCG | CGC | TCG | CAG | CGG | CGG | GGT | AGG | ACT | 1440 |
| Thr | Val | Pro | Gln | Asp | Ala | Val | Ser | Arg | Ser | Gln | Arg | Arg | Gly | Arg | Thr |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |      |
| GGC | AGG | GGT | AGG | AGA | GGC | ATC | TAC | AGG | TTT | GTG | ACT | CCG | GGA | GAA | CGG | 1488 |
| Gly | Arg | Gly | Arg | Arg | Gly | Ile | Tyr | Arg | Phe | Val | Thr | Pro | Gly | Glu | Arg |      |
|     |     |     |     | 485 |     |     |     | 490 |     |     |     |     | 495 |     |     |      |
| CCC | TCG | GGC | ATG | TTC | GAT | TCC | TCG | GTC | CTG | TGT | GAG | TGC | TAT | GAC | GCG | 1536 |
| Pro | Ser | Gly | Met | Phe | Asp | Ser | Ser | Val | Leu | Cys | Glu | Cys | Tyr | Asp | Ala |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |
| GGC | TGT | GCT | TGG | TAC | GAG | CTC | ACC | CCC | GCC | GAG | ACC | TCG | GTT | AGG | TTG | 1584 |
| Gly | Cys | Ala | Trp | Tyr | Glu | Leu | Thr | Pro | Ala | Glu | Thr | Ser | Val | Arg | Leu |      |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |
| CGG | GCC | TAC | CTG | AAC | ACA | CCA | GGG | TTG | CCC | GTT | TGC | CAG | GAC | CAC | CTG | 1632 |
| Arg | Ala | Tyr | Leu | Asn | Thr | Pro | Gly | Leu | Pro | Val | Cys | Gln |     |     |     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TTC | TTG | TCC | CAG | ACC | AAG | CAG | GCA | GGA | GAC | AAC | TTC | CCC | TAC | CTG | GTA | 1728 |
| Phe | Leu | Ser | Gln | Thr | Lys | Gln | Ala | Gly | Asp | Asn | Phe | Pro | Tyr | Leu | Val |      |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| GCA | TAC | CAA | GCC | ACG | GTG | TGC | GCC | AGG | GCT | CAG | GCC | CCA | CCT | CCA | TCA | 1776 |
| Ala | Tyr | Gln | Ala | Thr | Val | Cys | Ala | Arg | Ala | Gln | Ala | Pro | Pro | Pro | Ser |      |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| TGG | GAT | CAA | ATG | TGG | AAG | TGT | CTC | ATA | CGG | CTG | AAA | CCT | ACG | CTG | CAC | 1824 |
| Trp | Asp | Gln | Met | Trp | Lys | Cys | Leu | Ile | Arg | Leu | Lys | Pro | Thr | Leu | His |      |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| GGG | CCA | ACA | CCC | TTG | CTG | TAC | AGG | CTG | GGA | GCC | GTC | CAA | AAT | GAG | GTC | 1872 |
| Gly | Pro | Thr | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Ala | Val | Gln | Asn | Glu | Val |      |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| ACC | CTC | ACC | CAC | CCC | ATA | ACC | AAA | TAC | ATC | ATG | GCA | TGC | ATG | TCG | GCC | 1920 |
| Thr | Leu | Thr | His | Pro | Ile | Thr | Lys | Tyr | Ile | Met | Ala | Cys | Met | Ser | Ala |      |
|     | 625 |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| GAC | CTG | GAG | GTC | GTT | ACG | TAG | GAA | TTC | GAG | CTC | CGT | CGA | CAA | GCT | TGC | 1968 |
| Asp | Leu | Glu | Val | Val | Thr | *   | Glu | Phe | Glu | Leu | Arg | Arg | Gln | Ala | Cys |      |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| GGC | CGC | ACT | CGA | GCA | CCA | CCA | CCA | CCA | CCA | CTG | AGA | TCC |     |     |     | 2007 |
| Gly | Arg | Thr | Arg | Ala | Pro | Pro | Pro | Pro | Pro | Leu | Arg | Ser |     |     |     |      |
|     |     |     |     | 660 |     |     |     | 665 |     |     |     |     |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: RNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCUCGCCCCGG GGAUCCUCUA GGAAUACACG UUCGAU 36

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: RNA (genomic)

CUAGAGGAUC CCCGGGCGAG CCCUAUAGUG AGUCGU 36

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

GCTCGCCCGG GGATCCTCTA G 21